

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2003, 18:54:36 ; Search time 85 Seconds
(without alignments)
1216.890 Million cell updates/sec

Title: US-09-954-936-2
Perfect score: 2703
Sequence: 1 MRCSPGVWLAASLLHVS.....TIGILMSAPNFVEAVSKDFA 502

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2546	94.2	502	11 - Q9JHD6	Q9jhd6 mus musculus
2	1816.5	67.2	511	13 Q03481	Q03481 gallus gall
3	1260	46.6	807	5 Q8T7V5	Q8t7v5 drosophila
4	1254.5	46.4	501	5 Q9X2I4	Q9x2i4 heliothis v
5	1242	45.9	496	5 Q9X2I3	Q9x2i3 heliothis v
6	1221	45.2	494	5 Q8T7S2	Q8t7s2 drosophila
7	1219	45.1	494	5 Q8T7S3	Q8t7s3 drosophila
8	1214	44.9	494	5 Q8T7S1	Q8t7s1 drosophila
9	1204.5	44.6	509	5 Q8T7S0	Q8t7s0 drosophila
10	1202.5	44.5	523	5 Q8T7R9	Q8t7r9 drosophila
11	1093	40.4	554	5 Q62083	Q62083 caenorhabdi
12	998	36.9	461	5 P91197	P91197 caenorhabdi
13	972.5	36.0	523	5 Q46128	Q46128 heliothis v
14	954	35.3	311	5 Q9VW18	Q9vw18 drosophila
15	950.5	35.2	545	5 Q96631	Q96631 heliothis v
16	949.5	35.1	568	5 Q9NFR5	Q9nfr5 drosophila

17	947.5	35.1	536	5 Q8T0Y9	Q8t0y9 aplysia cal
18	947	35.0	515	5 Q46133	Q46133 locusta mig
19	944	34.9	542	5 Q18556	Q18556 caenorhabdi
20	941.5	34.8	552	5 P91765	P91765 myzus persi
21	938.5	34.7	537	5 Q8U941	Q8u941 myzus persi
22	937.5	34.7	536	5 Q8T9S0	Q8t9s0 aplysia cal
23	933	34.5	512	11 Q91X60	Q91x60 mus musculu
24	925.5	34.2	580	5 Q9VC72	Q9vc72 drosophila
25	921	34.1	629	11 Q9ET51	Q9et51 mus musculu
26	920	34.0	495	11 Q8R493	Q8r493 mus musculu
27	920	34.0	795	5 O18394	O18394 drosophila
28	919	34.0	629	11 Q923N8	Q923n8 mus musculu
29	919	34.0	641	11 Q923N7	Q923n7 mus musculu
30	917.5	33.9	499	11 Q8VHR6	Q8vhr6 mus musculu
31	917	33.9	502	5 Q9N587	Q9n587 caenorhabdi
32	915	33.9	540	5 O46134	O46134 locusta mig
33	914.5	33.8	499	11 Q8R4G9	Q8r4g9 mus musculu
34	907	33.6	531	5 Q96632	Q96632 heliothis v
35	907	33.6	595	5 P91764	P91764 myzus persi
36	897.5	33.2	452	13 Q918C7	Q918c7 gallus gall
37	894	33.1	496	6 Q8SPU6	Q8spu6 bos taurus
38	894	33.1	533	5 Q8WRS1	Q8wrs1 chilo suppr
39	886	32.8	772	5 Q9W3G6	Q9w3g6 drosophila
40	885	32.7	776	5 Q42202	Q42202 drosophila
41	883.5	32.7	517	5 Q96633	Q96633 heliothis v
42	877	32.4	509	5 Q9NFX8	Q9nfx8 myzus persi
43	876.5	32.4	547	5 Q8WSF9	Q8wsf9 aplysia cal
44	876	32.4	497	5 O46135	O46135 locusta mig
45	874	32.3	494	11 Q9R0W9	Q9r0w9 mus musculu

ALIGNMENTS

RESULT 1

Q9JHD6 PRELIMINARY; PRT; 502 AA.

ID Q9JHD6; AC Q9JHD6; DT 01-OCT-2000 (TREMREL. 15, Created) DT 01-OCT-2000 (TREMREL. 15, Last sequence update) DT 01-JUN-2002 (TREMREL. 21, Last annotation update) DE Nicotinic acetylcholine receptor subunit alpha 7. GN CHRNA7. OS Mus musculus (Mouse). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. OX NCBI_taxid=10090; [1] RN SEQUENCE FROM N.A. RP STRAIN=DBA/21BG; RC MEDLINE=97189245; PubMed=9037516; RA Stitzel J.A., Farnham D.A., Collins A.C.; RT "Linkage of strain-specific nicotinic receptor alpha 7 subunit restriction fragment length polymorphisms with levels of alpha-bungarotoxin binding in brain"; RL Brain Res. Mol. Brain Res. 43:30-40 (1996).

[2] RN SEQUENCE FROM N.A. RP STRAIN=DBA/21BG; RC MEDLINE=97189245; PubMed=9037516; RA Stitzel J.A.; RT "Linkage of strain-specific nicotinic receptor alpha 7 subunit restriction fragment length polymorphisms with levels of alpha-bungarotoxin binding in brain"; RL Brain Res. Mol. Brain Res. 43:30-40 (1996).

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY). CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY. DR EMBL; AF225980; AA35885.1; -. DR MGD; MG1:99779; Chrna7. DR InterPro; IPR000188; GABAA receptor. DR InterPro; IPR001175; Neur Channel. DR Pfam; PF02931; Neur_chan_LBD; 1. DR Pfam; PF02932; Neur_chan_memb; 1. DR PRINTS; PR00252; NRIONCHANNEL. DR TIGRFAMS; TIGR00860; LIC; 1. DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1. KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;

KW Transmembrane.
SQ SEQUENCE 502 AA; 56617 MW; C9353E5136D620E3 CRC64;
Query Match 94.2%; Score 2546; DB 11; Length 502;
Best Local Similarity 93.8%; Pred. No. 3.2e-217;
Matches 466; Conservative 19; Mismatches 12; Indels 0; Gaps 0;
QY 6 GGWLALAAALLHVSLLQGEFORLYKELVKNYNPLRPVANDSOPLTVYFSLSLQIMDV 65
Db 6 GGWLALAAALLHVSLLQGEFORLYKELVKNYNPLRPVANDSOPLTVYFSLSLQIMDV 65
QY 66 DEKNQVLTNIWLQMSWTDHYLQWNVSEYPGVKTVPDGOIKWPDILLNYSADDERFAT 125
Db 66 DEKNQVLTNIWLQMSWTDHYLQWNVSEYPGVKNVFPDGOIKWPDILLNYSADDERFAT 125
QY 126 FHTNVLVNSGHCYOYLPPIGIFKSSCYIDVRWFPDVOHCKLKFGSWSYGWSLDLQOE 185
Db 126 FHTNVLVNSGHCYOYLPPIGIFKSSCYIDVRWFPDVOHCKLKFGSWSYGWSLDLQOE 185
QY 186 DISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPDTFTVMRRRTLYYGLNLLIPCVLIS 245
Db 186 DISSYIPNGEWDLVGIPGKRSEFYECCKEYPDPDTFTVMRRRTLYYGLNLLIPCVLIS 245
QY 246 ALALLVFLPADSGEKISLITVLLSLTFMLLVAEIMPATSDSVPLIAQYFASTMIIVG 305
Db 246 ALALLVFLPADSGEKISLITVLLSLTFMLLVAEIMPATSDSVPLIAQYFASTMIIVG 305
QY 306 LSVVTVIVLYHHHPDGGKMPKWTIVLLNWCWFLMRKRPDQKVRPACQKQRCS 365
Db 306 LSVVTVIVLYHHHPDGGKMPKWTIVLLNWCWFLMRKRPDQKVRPACQKQRCS 365
QY 366 LASVENSAPPASNGNLVYIGRGLDGVHCVPTDPSGVVCGRMACSPHDEHLHGGQ 425
Db 366 LASVELSAGAPSSNGNLVYIGRGLGHECAPDPSGVVCGRLACSPHDEHMGTH 425
QY 426 PPEGDPDLAKILBEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFIICTIG 485
Db 426 PSDGDPDLAKILBEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFIICTIG 485
QY 486 ILMSAPNFVEAVSKDFA 502
Db 486 ILMSAPNFVEAVSKDFA 502

RESULT 2
Q03481 PRELIMINARY; PRT; 511 AA.
AC Q03481;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Alpha8 subunit of nicotinic acetylcholine receptor precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=90315158; PubMed=2369519;
RA Schoepfer R., Conroy W.G., Whiting P., Core M., Lindstrom J.;
RT "Brain alpha-bungarotoxin-binding protein cDNAs and mAbs reveal
subtypes of this branch of the ligand-gated ion channel gene
superfamily.";
RT Neuron 5:35-48(1990).
RL Neuron 5:35-48(1990).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR ENBL; X52296; CAA36544.1;
DR InterPro; IPR001188; GABA_A receptor.
DR InterPro; IPR001175; Neur channel.
DR Pfam; PF02931; Neur_chan_IAD; 1.
DR Pfam; PF02932; Neur_chan_nemb; 1.

DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor; Signal;
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 511 POTENTIAL.
SQ SEQUENCE 511 AA; 58705 MW; 10F362D153EC87A7 CRC64;
Query Match 67.2%; Score 1816.5; DB 13; Length 511;
Best Local Similarity 68.8%; Pred. No. 1.6e-152;
Matches 342; Conservative 56; Mismatches 94; Indels 5; Gaps 4;
QY 8 VWLALAAALLHVSLLQGEFORLYKELVKNYNPLRPVANDSOPLTVYFSLSLQIMDVDE 67
Db 16 LWASLFLSFPFKVQSGESQRLYRDLLRNYNELRPVANDSOPIVVELQSLQIIVDE 75
QY 68 KNOVLTTNIWLQMSWTDHYLQWNVSEYPGVKTVPDGOIKWPDILLNYSADDERFATFH 127
Db 76 KNOVLITNWLQMSWTDHYLQWNVSEYPGVKTVPDGOIKWPDILLNYSADDERFATFH 135
QY 128 TNVLVNSGHCYOYLPPIGIFKSSCYIDVRWFPDVOHCKLKFGSWSYGWSLDLQOEADI 187
Db 136 TNVLVNSGHCYOYLPPIGIFKSSCYIDVRWFPDVOHCKLKFGSWTHSGWLDLQOEADI 195
QY 188 SGYIPNGEWDLVGIPGKRSEFYECCKEYPDPDTFTVMRRRTLYYGLNLLIPCVLISAL 247
Db 196 SNYLSNGEWDLVGIPGKRSEFYECCKEYPDPDTFTVMRRRTLYYGLNLLIPCVLISGL 255
QY 248 ALLVFLPADSGEKISLITVLLSLTFMLLVAEIMPATSDSVPLIAQYFASTMIIVGLS 307
Db 256 ALLVFLPADSGEKISLITVLLSLTFMLLVAEIMPATSDSVPLIAQYFASIMVIVGLS 315
QY 308 VVTVIVLYHHHPDGGKMPKWTIVLLNWCWFLMRKRPDQKVRPACQKQRCS 364
Db 316 VVTVIVLYHHHPDGGKMPKWTIVLLNWCWFLMRKRPDQKVRPACQKQRCS 374
QY 365 SLASVENSAPPASNGNLVYIGRGLDGVHCVPTDPSGVVCGRMACSPHDEHLHGG 424
Db 375 SLKNTMNVLPFGHPSNGNMIY-SYHTMENPCCQNNDLGSKGKITCPLSEDEHVKKK 433
QY 425 QPPEGDPDLAKILBEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFIICTI 484
Db 434 ALMOTIPVIVKILBEVQFIANFRKQDEGEIECSWKFAACVVDRLCLVATLFAICTF 493
QY 485 GILMSAPNFVEAVSKDFA 501
Db 494 TILMSAPNFVEAVSKDFA 510

RESULT 3
Q087V5 PRELIMINARY; PRT; 807 AA.
ID Q087V5
AC Q087V5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Nicotinic acetylcholine receptor Dalpha5 subunit.
GN NACRALPHA-34E.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21969411; PubMed=11973307;
RA Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
RT "Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
Mediated A-to-I Pre-mRNA Editing.";
RT Mediated A-to-I Pre-mRNA Editing.";
RL Genetics 160:1519-1533(2002).

[illegible]

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RESULT 4
Q9XZ14
ID Q9XZ14 PRELIMINARY; PRT; 501 AA.
AC O9XZ14;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, last annotation update)
DE Putative nicotinic acetylcholine receptor alpha 7-2 subunit.
OS Heliothis virescens (Noctuid moth) (Owlet moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Noctuoidea; Noctuidae; Heliothinae; Heliothis.
OC NCBI_TaxID=7102;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte T., Oellers N., Adamczewski M.;
RT "Putative alpha subunits of insect nicotinic acetylcholine receptors
RT more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than
RT to other insect nicotinic acetylcholine receptor alpha subunits.";
RL Submitted (APR-1999) to the ENBL/GenBank/DBSJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR ENBL; AF143847; AA032698.1; -.
DR InterPro; IPR000188; GABA_A_receptor.
DR InterPro; IPR001175; Neur_Channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.

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DR	TIGRFAMs; TIGR00860; LIC; 1.
DR	PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW	Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW	Transmembrane.
SQ	SEQUENCE 501 AA; 56704 MW; 43CB0DC3960C78AB CRC64;
Query Match	46.4%; Score 1254.5; DB 5; Length 501;
Best Local Similarity	48.4%; Pred. No. 1e-102;
Matches 249; Conservative	75; Mismatches 139; Indels 51; Gaps 7
OY	10 LALAASLLHVSLSQEFORFKLYELKVNYNPLRPVANDSQPIIVYFSLSLQLQIDVDSEKN 69
DB	8 LALLA-LUPVSEQPHEKRLNALLANTLURPVANESFELEVRFGUTLQQIIDVDSEKN 66
OY	70 QVLTTNIWLQMSWDHDVLQMWNVSEYPGVKTYFRFDGQIKWKPDIIILYNSADRRFATFTN 129
DB	67 QLLITNIWLSLEWDYNLRWDSYGGVKDLRIIPNLKWKPDVLMYNSADESGDGTQTN 126
OY	130 VLVNSSGHCHQLPPGIIFKSCYVIDRVMPFPDVQHCKLKFGSWSYGGWSLDLOMQE---AD 186
DB	127 VVVRSGSGCLYVPPIFKSTCKMDIAWPPFDQHCMDKFSGWTYDGNQLDLVLKEAGGD 186
OY	187 ISGYIPNGEWDLVIGPKGRSERFYECCKEPDYDTFTVTMRRTLYYGLNLLIPCVLISA 246
DB	187 LSDFITNGEWYLIGMGPKKNTITYACCPYVYDVTFTIMIRRTLYYFFNLIVPCVLISS 246
OY	247 LALILVFLPADSGEKISLGITVLISLTFTMLVAEIMPATSDSVPLIAQYEASTMIIVGL 306
DB	247 MALLGFILPPDSGEKLITGVITILLSLVFLNLVAETLPQVSDAIPLLCTYENCIMFWAS 306
OY	307 SVVVTVIVLYQHHHPDPGGKMKPWTRVILLNWCAWFLRMKPGEDKVRPAOCHKORRCSL 366
DB	307 SVULTVVVLYNHRTADITHEMPQWIKSVFLQWLPWILRMSRPGKKTKRTKMNTMRREL 366
OY	367 ASVEMSAVA-----PPP---ASNGLLIYIGRGLDGHVCHVCPTPDSGVVC 407
DB	367 ELKERSKSLLANVLDDDDFRHGPPPNPSTASTGNL-----GGPC 407
OY	408 G-----RMACSPTHDEHLHGGOPPEGDDPLAKILEEVRYIANRPRCODESEAVCEW 460
DB	408 SIFPTDFRFRVRESTDENV--GGGLSHRHRELHLIIRELOFIYARMKKADEAEILSDW 465
OY	461 KFAACVVDRLCLMAFSVFTTICTIGILMSAPNFV 494
DB	466 KFAAMVVDRCFLVFFTLTFTTIATVAVLLSAPHII 499
RESULT 5	
Q9XZ13	
ID	O9XZ13 PRELIMINARY; PRT; 496 AA.
AC	O9XZ13;
DT	01-NOV-1999 (TrEMBRel. 12, Created)
DT	01-JUN-1999 (TrEMBRel. 12, Last sequence update)
DT	01-JUN-2002 (TrEMBRel. 21, Last annotation update)
DE	Putative nicotinic acetylcholine receptor alpha 7-1 subunit.
OS	Heliothis virescens (Noctuid moth) (Owllet moth).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC	Noctuoidae; Noctuidae; Heliothinae; Heliothis.
RN	NCBI_TaxID=7102;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Schulte T., Oellers N., Adamczewski M.;
RT	"Putative alpha subunits of insect nicotinic acetylcholine receptors
RT	more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than
RT	to other insect nicotinic acetylcholine receptor alpha subunits."
RL	Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
CC	- - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC	- - SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR	EMBL; AF143846; AAD32697.1; -
DR	InterPro; IPR000188; GABAA_receptor.
DR	InterPro; IPR001175; Neur Channel.
DR	Pfam; PF02931; Neur chan IBD. 1.

Db	14	LLIFLAIKESQCGPHEKRLNLHLLSTYNTLRLPVRANESPELVFKGLTLQOIIDVDEKN	73
Qy	70	QVLTTNIWLQMSWTBHYLQWNVSEYPGVKTVRFPDGOIWKPDILLYNSADERFDATFHTN	129
Db	74	QLLITNLWLSLEWNDYNLRWNETEYGGVKDLRIITPNKLWKPDVLWYNSADEGFDGYHTN	133
Qy	130	VLVNSSGHCOYLPPGIGIKSSCYIDVRWPFDDVQHCKLKFSGWSYGLDQMQE---AD	186
Db	134	IVKHSGSCLYVPPGIFKSTCKMDITWFPDDQHCMEKFGSWTYDGNQLDLVNSEDDGD	193
Qy	187	ISGYIPNGEWDLVGTPGRSERFYECCKEPPDVTFTVMRRRTLYYGLNLILPCVLISA	246
Db	194	LSDFITNGEWYLLAMPGKKNTIVACCEPYVDITFIQIRRTLYYFENLIYVPCVLIS	253
Qy	247	LALLVELLLPADSGEKISLIGITVLLSTFTMLLVAEIMPATSDVPILIAQYFASTMIIVGL	306
Db	254	MALLGFTLPPDSGEEKITUGVTILLSTVFLNLVAETLPQVSDAIPLLGYFNCIMFPMVAS	313
Qy	307	SWVTVIVLQYHHDDPDGCKMPKTRVILLNWCAWFLMRKRGEDKVPACQHKQRCSL	366
Db	314	SVLTVVLVNYHRTADITHEMPPWKSVFLQWLPLWLRMGPRGRKTRKTILLSNEMKEL	373
Qy	367	ASVEMSAVAPPASNGNLLYI--GPRGLDGWCHVCTPDPGSGVVVCGRMACSPT--HDBHLHL	422
Db	374	ELKERS-----KSLIANVLIDDDDFR-----HTISGSQTAISSASFRGPTVEEHHTAI	424
Qy	423	GGQPPEGDPDLAKTILEEVRYIANRFRCODESEAVCSWKFAACVVDRLCMAFSPVETIIC	482
Db	425	GC-----NHKDLHLILKELQFITARMRKADDEAELIGDWKFAAMVVDRFCLIVFTLTFTIIA	480
Qy	483	TIGILMGPANFV	494
Db	481	TVTVLISAPHII	492
RESULT	9		
Obt7S0			

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RESULT 9
Q8T7S0
ID Q8T7S0 PRELIMINARY; PRT; 509 AA.
AC Q8T7S0;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Nicotinic acetylcholine receptor Dalpha6 subunit variant type IV.
GN NACRALPHA-30D.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21969411; PubMed=11973307;
RA Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
RT "Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
RT Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
RT New and Highly Conserved target of Adenosine Deaminase Acting on RNA-
RT Mediated A-to-I Pre-mRNA Editing.";
RL Genetics 160:1519-1533(2002).
DR EMBL: AF321448; AAM13395.1; -.
KW Receptor.
SQ SEQUENCE 509 AA; 57887 MW; BE8D8E0198E0C2BD CRC64;
Query Match 44.6%; Score 1204.5; DB 5; Length 509;
Best Local Similarity 46.2%; Pred. No. 2.8e-98;
Matches 234; Conservative 84; Mismatches 154; Indels 35; Gaps 7
Qy 10 LALAASLLHVSLOGEFORKYKEIVKXNNYPLERPVANDSQPLTYVFSLSLLQIMDVDEKN 69
Db 14 LLIFLAIIKESCCQPEKRLNLLSYNTLRLRPVANESEPLEVKFGLTLQQIIVDEKN 73
Qy 70 QVLT-----TNILQMSWTHYLOWNVSEYPGVTVTFPPDQIQIKPDILL 114
Db 74 QIITTNAMLNDEKNQLLIINLMSLEWNDYNLFWNETEYGGVKDLRITPNKLWKPDVIM 133

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QY 115 YNSADERFDATEHTNVLNNSGHCQYLPFGIFKSCYIDVRFPFVQVHCKLFGSWSYG 174
 DB 134 YNSADEGPDCTVHTNVIWKRSGCLVPPGIPKSTCKMDITWFPDDQHCMEKFGSWTYD 193
 QY 175 GWSLDLQOE---ADISGYPNGEWDLVGPGRSERFECCKEPPDVFTVTRRRL 231
 DB 194 GNQLDLVNSDGGDLSDFITNGEYLLAMPKGNKTIYVACCPYVDITFTIQRRL 253
 QY 232 YVGNLLIPCVLISALALLVFLPADSGEKISIGITVLLSLTTFMLLVAEIMPATSDSVP 291
 DB 254 YFFNLVPCVLISWALLGFTLPDSGEKLTGLVTLISLTVFLNLVAETLPOVSDAIP 313
 QY 292 LIAQYFASPMIIVGLSVVTVIVLQYHHDPDGGKMPKTRVILLNWKAFWLRMPGPD 351
 DB 314 LGLTYFNCIMFVASSVLTVVVLYNHRHTADHEMPWIKSVFLOLWPLWLRMPGRK 373
 QY 352 KVRPACQHKORCSLASVEMSAVAPPASNGNLLYI--GFRGLDGVHCVPTPDSGVVCGR 409
 DB 374 ITRKTILLSNRKLELKERSS---KSLANVLDDDDFR---HTISGSQTAGSSA 424
 QY 410 MACSP--HDEHLLHGQPEGPDPLAKILEEVRYIANRRCODESEAVCSEWKFACV 467
 DB 425 SFRGPTVEEHTAIGC---NHKDLHLILKELQFITARMRKADDEALIGDWKFAAMV 480
 QY 468 DRCLMAFSVFTIITIGILMSAPNFV 494
 DB 481 DRFCILVFTLITIAVTVLLSAPHII 507

RESULT 10

Q87R9
 ID Q87R9 PRELIMINARY; PRT; 523 AA.
 AC Q87R9;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Nicotinic acetylcholine receptor Dalpha6 subunit variant type V.
 GN NACRALPHA-30D.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21969411; PubMed=11973307;
 RA Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
 RT "Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes.
 RT Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster identify a
 RT New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
 RT Mediated A-to-I Pre-mRNA Editing.";
 RL Genetics 160:1519-1533(2002).
 DR EMBL; AF321449; AAM13396.1; .
 KW Receptor.
 SQ SEQUENCE 523 AA; 59110 MW; 1C200AF74F87F841 CRC64;

Query Match 44.5%; Score 1202.5; DB 5; Length 523;
 Best Local Similarity 45.5%; Pred. No. 4.4e-98;
 Matches 237; Conservative, 81; Mismatches 154; Indels 49; Gaps 7;
 QY 10 LALAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSOPLTVYFSLQIQMDVDEKN 69
 DB 14 LLIFLAIKESQCPHEKRLNHLSTYNTLERPVANSEPLEYKGLTLQIQIIVDEKN 73
 QY 70 QVLTNMIWOMSWTDHYLQWNVSEYPCVKTVPDGOIWKPDILLYNSADERFDATEHTN 129
 DB 74 QIUTTNWNLNLEWNYLRNWEYGGVKDLRITPNKWLKPDVLYNSADEGPDGTHTN 133
 QY 130 VLVNNSGHCQYLPFGIFKSCYIDVRFPFVQVHCKLFGSWSYGGWSLDLQOE---AD 186
 DB 134 IVVKNHSGCLVPPGIFKSTCKMDITWFPDDQHCMEKFGSWTYDGNQLDLVNSDGGD 193

QY 187 ISGYIPNGEWDLVGIPIGKRSEFYECCKEPPDVFTVTRRRLTYVGLNLLIPCVLISA 246
 DB 194 LSDFITNGEYLLAMPKGNKTIYVACCPYVDITFTIQRRLTYVFFNLVPCVLISS 253
 QY 247 LALLVFLPADSGEKISIGITVLLSLTTFMLLVAEIMPATSDSVP 293
 DB 254 MALLGFTLPDSGEKLTGLVTLISLTVFLNLVAESMPTTSDAVPLIGVTLISLTVFLN 313
 QY 294 -----AQYFASPMIIVGLSVVTVIVLQYHHDPDGGKMPKTRVILLN 337
 DB 314 LVAETLPOVSDAIPLGLTYFNCIMFVASSVLTVVVLYNHRHTADHEMPWIKSVFLO 373
 QY 338 WCWAFWLRMPGPDKVRPACQHKORCSLASVEMSAVAPPASNGNLLYI--GFRGLDGV 395
 DB 374 WLPWILRMGRPKRITKRTILLSNRKLELKERSS---KSLANVLDDDDFR----- 424
 QY 396 HCVPTPDSGVVCGMACSP--HDEHLLHGQPEGPDPLAKILEEVRYIANRRCODES 453
 DB 425 HTISGSQTAGSSASFRGPTVEEHTAIGC---NHKDLHLILKELQFITARMRKADDE 480
 QY 454 EAVCSEWKFACVVDRLCLMAFSVFTIITIGILMSAPNFV 494
 DB 481 AELIGDWKFAAMVVDRECLVFTLITIAVTVLLSAPHII 521

RESULT 11

O62083
 ID O62083 PRELIMINARY; PRT; 554 AA.
 AC O62083;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE C31H5.3 protein.
 GN C31H5.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kershaw J.K.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL; Z93778; CAB07843.2; .
 SQ SEQUENCE 554 AA; 63286 MW; E4F056B2B660A992 CRC64;

Query Match 40.4%; Score 1093; DB 5; Length 554;
 Best Local Similarity 40.6%; Pred. No. 2.4e-88;
 Matches 224; Conservative, 94; Mismatches 160; Indels 74; Gaps 8;
 QY 8 VWLALAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSOPLTVYFSLQIQMDVDE 67
 DB 7 IGIAFFALFRVITGDERRLYAKLAENYNKLARPVNRSEAVVVLGMDYQQILDIDE 66
 QY 68 KNOVLTNMIWOMSWTDHYLQWNVSEYPCVKTVPDGOIWKPDILLYNSADERFDATEHTN 127
 DB 67 KHQIMNWNVLRMSTWTDHYLQWNVSEYPCVKTVPDGOIWKPDILLYNSADERFDATEHTN 126
 QY 128 TNVLNNSGHCQYLPFGIFKSCYIDVRFPFVQVHCKLFGSWSYGGWSLDLQOEADI 187
 DB 127 VNAVLYTGNVTWIPPAIRSSCAIDIAFFPDIOHCTKFGSWTYSGFFDLINTISP 186
 QY 188 SGYIPNGEWDLVGIPIGKRSEFYECCKEPPDVFTVTRRRLTYVGLNLLIPCVLISA 247
 DB 187 ATYKPNGEWELLGLTSQRSIFFECCPEPYVDITFTVIRRLTYVGFNLLPCMLISSL 246
 QY 248 ALLVFLPADSGEKISIGITVLLSLTTFMLLVAEIMPATSDSVP 307

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Db 247 ALLSFTLPADCGEKLNGVTIFMSLCVFMIMVAEMPQTSALPLIQIFYFSCIMFQVGAS 306
Qy 308 VVVTVIVLQVHHDDPGGK-MPKWTRVILLNWCWFLMRKPPGDKVRPAQH-----K 360
Db 307 VVATVIALNPHRRSPQYKPMNKFLKTLILGWLPTLLGMRPDLVLSVHGHAHYASDNKK 366
Qy 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLD-----393
Db 367 KORQYLIEVERHILTRP---NGN-----GHSVADKAVHLDLSTGNPHDASKSPSPKRTS 419
Qy 394 ----GVHCVTP-----DSGV---VCGRMACSPTHDEHLLHGGQPPGDDP-----431
Db 420 ASIMGWTLPTTQWNGALDSSINKYCTKVTREPLNGSAINHKSSQFINNNNIYKC 479
Qy 432 -----DLAKILEEVRYIANFRCODESEAVCSWKFAACVVDRCLCLMAFSVFTI 480
Db 480 ANNQKTFQEDRPHHILNELRVISARVRKEEMHALQADWMAFASRVDRVCFLAFAFLF 539
Qy 481 ICTIGILMSAPN 492
Db 540 MCTAIIISYNAPH 551

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RESULT 12

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P91197
ID P91197 PRELIMINARY; PRT; 461 AA.
AC P91197;
DT 01-MAY-1997 (T-EMBLrel. 03, Created)
DT 01-MAY-1997 (T-EMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Hypothetical 52.7 kDa protein.
GN D2092.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Gattung S., Maggi L.;
RT "The sequence of C. elegans cosmid D2092.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC EMBL; U88167; AAB42223.1; -
DR InterPro; IPR000188; GABAA_receptor.
DR InterPro; IPR001175; Neur_chan_1.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRfam; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Hypothetical protein; Ionic channel;
KW Postsynaptic membrane; Transmembrane.
SQ SEQUENCE 461 AA; 52718 MW; 6182AF827357B92 CRC64;
Query Match 36.9%; Score 998; DB 5; Length 461;
Best Local Similarity 39.8%; Pred. No. 5.1e-80;

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Matches 197; Conservative 96; Mismatches 146; Indels 56; Gaps 8;
Qy 12 LAASLLHSL-OGSF-ORLYKELVKNYNPLRPVANDSOPLTVVFSLLQIMVDEN 69
Db 10 LSLVIIHSLNCDGSAETKLTDLKGYNPLRPVQNSOPLKIKLFLOQLDVEN 69
Qy 70 OVLTTNIWLSWTDHYLQWNVSEYGVKTVRF--DGIWKPDILLNSADDERDATEH 127
Db 70 QIVSVNAWLSYTWFDHKLQWEPKYGQIDIRFGSSDHIWKPDVLLYNSAAEDFDSTPK 129
Qy 128 TNVLVNSGHCQYLPPGIFKSCYIDVRWFFDVQHCKLFGKGSWSYGSMSLDLQW- 182
Db 130 SNLLTYHTGTWVTPPGVLKFCQLDVTWFFDDQVCEMKFGSWTFHGYAIDLQDDDTN 189
Qy 183 --QADISGYIPNGEWDLVGIPKRSERFYCKEPEYDPVTVTMRRTLYYGNLLIP 240
Db 190 GTQMDLSTYLNGEWOVISTNAKRVSVYKCCPEYPTVNYLHRRRTLYYGNLLIP 249
Qy 241 CVLISALALLFLLPADSGEKISLIGITVLLSLTFLMLVAIMPATSDSVLIAQYFAST 300
Db 250 SLLISLMAILGFMPPDAGEKITLEVITLLAIVFVFLSMVSEMTPTSEAVPLIGVFFSC 309
Qy 301 MIIVGLSVVTVIVLQVHHDDPGCKMPKTRVILLNWCWFLMRKPPGDKVRPAQH 360
Db 310 MLVSVASVTVIIVNLHFRSADSHENMPLVRRLEFLPMLFMRGKYFVK-----363
Qy 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPT-TPDSGVVCGRMACSPTHDEH 419
Db 364 ----ANV-----IDSTDKMPKPKNPLDCLNPSNHAGYEAQ 395
Qy 420 LHHGGQPPGDDLAKILEEVRYIANFRCODESEAVCSWKFAACVVDRCLCLMAFSVFT 479
Db 396 ILL-----LHSHVTELRVVAFYNKHEEDERIQDWRFAAMVVDRACLLFTVFI 445
Qy 480 ICTIGILMSAPNEV 494
Db 446 VISILAIMMSAPHII 460

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RESULT 13

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O46128
ID O46128 PRELIMINARY; PRT; 523 AA.
AC O46128;
DT 01-JUN-1998 (T-EMBLrel. 06, Created)
DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Nicotinic acetylcholine receptor alpha subunit precursor.
GN NACHR.
OS Heliothis virescens (Noctuid moth) (Owlet moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pieriygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Noctuoidea; Noctuidae; Heliothinae; Heliothis.
OX NCBI_TaxID=7102;
RN [1]
RP SEQUENCE FROM N.A.
RA JafariGorzini S., Maelicke A.;
RT "Preliminary: Cloning of nicotinic acetylcholine receptor subunits of
Heliothis virescens.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL; AJ000399; CAA04056.1; -
DR InterPro; IPR000188; GABAA_receptor.
DR InterPro; IPR001175; Neur_chan_1.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR PRINTS; PR00232; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRfam; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor; Signal;
KW Transmembrane.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 523 NICOTINIC ACETYLCHOLINE RECEPTOR.

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50	SEQUENCE	523 AA; 59214 MW; 7E39A035B6BA00FD CRC64;	
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	Best Local Similarity	40.4%; Pred. No. 1.le-77;	
	Matches	209; Conservative 90; Mismatches 173; Indels 45; Gaps 11	
Qy	2	RCSP---GGWALAAASLLHVSLOGEFORKLYKELVKYNPLERPVANDSQPLTYVFSLS	58
Db	4	RAAPHRAGPLLLLVALAALACGAANPDAKRLYYDLLSNYNKLVRLVNLVSALTVRIKLK	63
Qy	59	LLQIMDVDEKNOVLTTNIWLQMSWTDHYLQWNVSEYPCGKTVKRPDPGOIKWKPDIILLYNSA	118
Db	64	LSQLIDVNLKNOIMTNNLWFSQSWDYKLSWEPREYGGVEMLHVPSDHIWRPDIVLYNNA	123
Qy	119	DEREDATFHTNVLNVSSGHCOYLPPIGIPKSCYIDVRWFPFDVQHQCKLKFGSWSYCGWSL	178
Db	124	DGNEVTLATKATILNYTGRVWRPPALYKSSCEIDVEYFPFDQQTQCNMKFGSWTYDGFQV	183
Qy	179	DLO-MQEA-----DISGYPNGSWDLVGIPICKRSERFYECKEPPYDVTVTVMR	227
Db	184	DLRHIDEARGTNVVELGVDLSEFYTSVSWDILEVPAVNEKRYTCDEPYLDITFNITMR	243
Qy	228	RRTLYGNNLLIPCVLISALALLVPLPADSGEKISIGITVLLSLTTMLLVAEITMPTS	287
Db	244	RKTLFYTVNLIIPCWGISFLVILVFLYPLSDSGEKVLSISILLSLTVFELLAEIIPTS	303
Qy	288	DSVPLIIAQFYASTMIIIVGLSVVVTVVILVOYHHDDPGGKMPKWTNRVILLNCAWFMRKR	347
Db	304	LWPELLGKFLVLTMLTDFSCVTWVLNVHFRSPQTHMAPVWRVRVTHVLPRLVNMRR	363
Qy	348	PGEDKVRPACOHKORRCSL-ASVMSAVAPPASNGNLLYTGFRGLDGVCHVCPTPDSGVV	406
Db	364	P-HYKVDP---HRSFAGLVTAVSESA---PWEDGSPGLAGLGAGPG---PPEP-----A	408
Qy	407	CGRMACSPTHDEHLHGQPPGD-----PDLAKILEEVRVYIANFRCODESEAVCS	458
Db	409	CAACRSCRHLD-----APALCDALRRWHRCPELNAKDINGINYAEQTRKEEESTRVKE	461
Qy	459	BWKFAACVVDRLCLMAFSVFTIICITIGILMSAPNFVE	495
Db	462	DKWYAMVLDRLFIMFTLAVVVGAGIILOAQTLYD	498

RESULT 14	
Q9VWI8	PRELIMINARY; PRT; 311 AA.
ID	
AC	O9VWI8;
DT	01-MAY-2000 (TRENBLrel. 13, Created)
DT	01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE	01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE	CG8109 protein.
GN	CG8109.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_taxID=7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BERKELEY;
RX	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA	Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA	wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA	Abiril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA	Balieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA	Besson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA	Borkova D., Botchan M.R., Bouck J.P., Brokstein P., Brotter P.,
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA	Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA	De
DB	GGVWLAALAAALL--HVSLOGEFORKLYKELVKYNPLERPVANDSOPLTVYFSLSLQI 62
DB	GGRLVVYGLGLIMI PACAAGPHEKRLLHALLDNYNSLERPVNVESDPLQLSFGTLMQI 75
QY	MDVDEKNQVLTTNIWLQMSWTDHYLQWNVSVEYPGKVTRPPDGQIWKPDIILYNSADERF 122
DB	IDVDEKNQLITINILWKLEWMNMNLRWNSSEFFGVGRDLIRIPPHRLKWPKDVMLYNSADEGF 135
QY	DATFTTNLVNSSGHCOYLPGPIFKSCYIDVRFPDFVDVOCHKLFKGSWSVGXSLDIQM 182
DB	DGTATNVNRVNRNSCLYVPFGIFRSTCKIDITWPFDDQCCEMKFGSWITDYGQLDQL 195
QY	QE---ADISGIYPNGEWDLVGPGRSRERFYECCKEPDPVTFTVRRRTLYYGLNLI 239
DB	QDEAGDISFITNGEWDLGLVPGKRNEIYNCPEPYDITFAILLRKTYFFFNLIIV 255
QY	PCVLISALALLVFLLPADSGEKISLGITVLTSLLTFMMLVAEIMPATSDSVPLIAQ 295
DB	PCVLIASMALLGFTLPDPSGEKLSLGVITILLSLTVFLNMVAETWPATSDAVPLLKG 311
RESULT 15	
O96631	PRELIMINARY; PRT; 545 AA.
ID	O96631;
AC	O96631;
DT	01-MAY-1999 (TRENBLrel. 10, Created)
DT	01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT	01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE	Nicotinic acetylcholine receptor alpha-2 subunit.
OS	Heliethis vitescens (Noctuid moth) (Owlet moth).

Search completed: June 20, 2003, 19:00:26
Job time : 89 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2003, 18:57:06 ; Search time 27 Seconds
(without alignments)
547.048 Million cell updates/sec

Title: US-09-954-936-2

Perfect score: 2703

Sequence: 1 MRCSPGGVWLALASLLHVS.....TIGILMSAPNFVEAVSKDFA 502

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*

2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*

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6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2703	100.0	502	4	US-08-771-737-2
2	2698	99.8	502	2	US-08-466-589-8
3	2698	99.8	502	2	US-08-700-636-8
4	2698	99.8	502	3	US-08-467-574-8
5	2698	99.8	502	4	US-09-217-345-8
6	2698	99.8	502	4	US-08-487-596-12
7	2540	94.0	502	1	US-08-278-635B-7
8	2540	94.0	502	3	US-08-464-258B-7
9	2540	94.0	502	3	US-08-471-961-7
10	1816.5	67.2	511	1	US-08-278-635B-8
11	1816.5	67.2	511	3	US-08-464-258B-8
12	1816.5	67.2	511	3	US-08-471-961-8
13	945	35.0	529	1	US-08-496-855A-2
14	945	35.0	529	4	US-08-487-596-2
15	943	34.9	510	1	US-08-278-635B-4
16	943	34.9	510	3	US-08-471-961-4
17	940.5	34.8	511	3	US-08-464-258B-4
18	920.5	34.1	528	2	US-08-466-589-2
19	920.5	34.1	528	2	US-08-700-636-2
20	920.5	34.1	528	3	US-08-467-574-2
21	920.5	34.1	528	4	US-09-217-345-2
22	908	33.6	504	2	US-08-466-589-4
23	908	33.6	504	2	US-08-700-636-4
24	908	33.6	504	3	US-08-467-574-4
25	908	33.6	504	3	US-09-217-345-4
26	905.5	33.5	629	1	US-08-278-635B-6
27	905.5	33.5	629	3	US-08-464-258B-6

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30	894	33.1	497	3	US-08-464-258B-5	Sequence 5, Appli
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33	884	32.7	498	4	US-08-487-596-18	Sequence 18, Appli
34	882	32.6	504	4	US-08-487-596-4	Sequence 4, Appli
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37	871	32.2	627	3	US-08-467-574-6	Sequence 6, Appli
38	871	32.2	627	4	US-09-217-345-6	Sequence 6, Appli
39	869	32.1	498	1	US-08-496-855A-6	Sequence 6, Appli
40	869	32.1	498	2	US-08-466-589-12	Sequence 12, Appli
41	869	32.1	498	2	US-08-700-636-12	Sequence 12, Appli
42	869	32.1	498	3	US-08-467-574-12	Sequence 12, Appli
43	869	32.1	498	4	US-09-217-345-12	Sequence 12, Appli
44	867.5	32.1	494	4	US-08-487-596-10	Sequence 10, Appli
45	861	31.9	502	2	US-08-466-589-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1

US-08-771-737-2

; Sequence 2, Application US/08771737

; Patent No. 6323000

; GENERAL INFORMATION:

; APPLICANT: Briggs, Clark A.

; APPLICANT: Gopalakrishnan, Murali

; APPLICANT: McKenna, David G.

; APPLICANT: Monteggia, Lisa M.

; APPLICANT: Roch, Jean-Marc

; APPLICANT: Sullivan, James P.

; APPLICANT: Touma, Edward

; APPLICANT: Abbott Laboratories

; TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE

; FILE OF INVENTION: RECEPTOR SUBUNIT, AND METHODS OF PRODUCTION AND USES THEREOF

; FILE REFERENCE: 6017 US 01

; CURRENT APPLICATION NUMBER: US/08/771,737

; CURRENT FILING DATE: 1996-12-20

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 502

; TYPE: PRT

; ORGANISM: homo sapien

US-08-771-737-2

Query Match 100.0%; Score 2703; DB 4; Length 502;

Best Local Similarity 100.0%; Pred. No. 4.6e-274; Mismatches 0; Indels 0; Gaps 0;

Matches 502; Conservative 0;

Qy	1	MRCSPGGVWLALASLLHVS	QGFQRLKYLKLVNPNL	RPVANDSOPLTVYFSL	60
Db	1	MRCSPGGVWLALASLLHVS	QGFQRLKYLKLVNPNL	RPVANDSOPLTVYFSL	60
Qy	61	QIMDVEKNQVLTNNI	WQMSWTDRHYLQWNS	YSEYPGVKTVPDQGI	WKPDI
Db	61	QIMDVEKNQVLTNNI	WQMSWTDRHYLQWNS	YSEYPGVKTVPDQGI	WKPDI
Qy	121	RFDATFTNNLVN	SGHCQYLP	PGIFKSSCS	YDVRWFFDVQHC
Db	121	RFDATFTNNLVN	SGHCQYLP	PGIFKSSCS	YDVRWFFDVQHC
Qy	181	QMQEADISGYIP	NGEWDLVGIP	GKRSEFYCCKE	PEYPDVFTVTMRRT
Db	181	QMQEADISGYIP	NGEWDLVGIP	GKRSEFYCCKE	PEYPDVFTVTMRRT
Qy	241	CVLISALALLV	FLPADSGEKIS	IGITVLLSLT	TFMLVAEIMPATSD
Db	241	CVLISALALLV	FLPADSGEKIS	IGITVLLSLT	TFMLVAEIMPATSD

QY 301 MIIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCAMFLRMKRPBGDKVRPACQHK 360
 Db 301 MIIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCAMFLRMKRPBGDKVRPACQHK 360
 QY 361 QRCCLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 Db 361 QRCCLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 QY 421 LHGGQPPGDPDLAKILEEVRYIANFRFCODESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 Db 421 LHGGQPPGDPDLAKILEEVRYIANFRFCODESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 2

US-08-466-589-8
 ; Sequence 8, Application US/08466589
 ; Patent No. 5837489
 ; GENERAL INFORMATION:
 ; APPLICANT: Elliot, Kathryn J.
 ; APPLICANT: Ellis, Steven B.
 ; APPLICANT: Harpold, Michael M.
 ; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
 ; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & McClaim
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92101-2926
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/466,589
 ; FILING DATE: June 5, 1995
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/028,031
 ; FILING DATE: March 8, 1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seidman, Stephanie L
 ; REGISTRATION NUMBER: 33,779
 ; REFERENCE/DOCKET NUMBER: 6362-9950
 ; TELEPHONE: 619-238-0999
 ; TELEFAX: 619-238-0062
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 502 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-08-466-589-8

Query Match 99.8%; Score 2698; DB 2; Length 502;
 Best Local Similarity 99.8%; Pred. No. 1.5e-273;
 Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MRCSPGGVWLAASLHVSLSQGFQRLKYELVKNYNPLRPVANDSQPLTVYFSLLL 60
 Db 1 MRCSPGGVWLAASLHVSLSQGFQRLKYELVKNYNPLRPVANDSQPLTVYFSLLL 60
 QY 61 QINDVDEKNQVLTNWLQSWTDHYLQWNVSEYPGVKTRVFPDQGIWKPDILLYNSADE 120

Db 61 QINDVDEKNQVLTNWLQSWTDHYLQWNVSEYPGVKTRVFPDQGIWKPDILLYNSADE 120
 QY 121 RFDATHTNVLNVSNGHCQYLPGIFKSSCVIVRWFPPDVQHCKLFGWSYSGWSL 180
 Db 121 RFDATHTNVLNVSNGHCQYLPGIFKSSCVIVRWFPPDVQHCKLFGWSYSGWSL 180
 QY 181 QMOEADISGYIPNGEWDLVGIPGKRSERFYECCKEYPPDVTFVTMRRRTLYYGLNLLIP 240
 Db 181 QMOEADISGYIPNGEWDLVGIPGKRSERFYECCKEYPPDVTFVTMRRRTLYYGLNLLIP 240
 QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFFMLLVABEIMPATSDSVPLIAQYFAST 300
 Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFFMLLVABEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCAMFLRMKRPBGDKVRPACQHK 360
 Db 301 MIIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCAMFLRMKRPBGDKVRPACQHK 360
 QY 361 QRCCLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 Db 361 QRCCLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 QY 421 LHGGQPPGDPDLAKILEEVRYIANFRFCODESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 Db 421 LHGGQPPGDPDLAKILEEVRYIANFRFCODESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 3

US-08-700-636-8
 ; Sequence 8, Application US/08700636
 ; Patent No. 5910582
 ; GENERAL INFORMATION:
 ; APPLICANT: Elliot, Kathryn J.
 ; APPLICANT: Ellis, Steven B.
 ; APPLICANT: Harpold, Michael M.
 ; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
 ; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
 ; STREET: 444 South Flower Street, Suite 2000
 ; CITY: Los Angeles
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 90071
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/700,636
 ; FILING DATE: 16-JUL-1996
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/028,031
 ; FILING DATE: 08-MAR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Reiter, Stephen E.
 ; REGISTRATION NUMBER: 31,192
 ; REFERENCE/DOCKET NUMBER: P41 9368
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-546-4737
 ; TELEFAX: 619-546-9392
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 502 amino acids
 ; TYPE: amino acid

;; STRANDEDNESS: single
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
US-08-700-636-8

Query Match 99.8%; Score 2698; DB 2; Length 502;
Best Local Similarity 99.8%; Pred. No. 1.5e-273;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAALASLLHVSILQGFQKLYKELVKNYNPLRPVANDSQPLTVVFSLSLL 60
DB 1 MRCSPGGVWLAALASLLHVSILQGFQKLYKELVKNYNPLRPVANDSQPLTVVFSLSLL 60
QY 61 QIMDVDEKNOVLTNIMLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120
DB 61 QIMDVDEKNOVLTNIMLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120
QY 121 RFDAFTHTNVLVNSGHCQYLPPIGIFKSSCYIDVRWPFDDVQHCCKLFGSWSYGGWSLDL 180
DB 121 RFDAFTHTNVLVNSGHCQYLPPIGIFKSSCYIDVRWPFDDVQHCCKLFGSWSYGGWSLDL 180
QY 181 QMQEADISGYIPNGEWDLVGIPIGKRSEFYECCKEYPDVTFTVTRRRTLYYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGIPIGKRSEFYECCKEYPDVTFTVTRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALALLVFLLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVIVLYQHHDDPGGKMPKTRVILLNCAWFLMRKRPGEKVRPACQHK 360
DB 301 MIIVGLSVVTVIVLYQHHDDPGGKMPKTRVILLNCAWFLMRKRPGEKVRPACQHK 360
QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
DB 361 QRCCLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
QY 421 LHGGQPEGDPDLAKILEEVRYIANFRQCDESAVCSWKFAACVVDRLCLMAFSVFTI 480
DB 421 LHGGQPEGDPDLAKILEEVRYIANFRQCDESAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 4

US-08-467-574-8
; Sequence 8, Application US/08467574
; Patent No. 6022704

GENERAL INFORMATION:

;; APPLICANT: Elliot, Kathryn J.
;; APPLICANT: Ellis, Steven B.
;; APPLICANT: Harpold, Michael M.
;; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
;; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Brown, Martin, Haller & McClaim
;; STREET: 1660 Union Street
;; CITY: San Diego
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 92101-2926

COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq Version 1.5
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/467,574
;; FILING DATE: June 5, 1995
;; CLASSIFICATION: 536

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/028,031
;; FILING DATE: March 8, 1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Seidman, Stephanie L.
;; REGISTRATION NUMBER: 33,779
;; REFERENCE/DOCKET NUMBER: 6362-9949
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-238-0999
;; TELEFAX: 619-238-0062
;; TELEX:

INFORMATION FOR SEQ ID NO: 8:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 502 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
US-08-467-574-8

Query Match 99.8%; Score 2698; DB 3; Length 502;
Best Local Similarity 99.8%; Pred. No. 1.5e-273;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAALASLLHVSILQGFQKLYKELVKNYNPLRPVANDSQPLTVVFSLSLL 60
DB 1 MRCSPGGVWLAALASLLHVSILQGFQKLYKELVKNYNPLRPVANDSQPLTVVFSLSLL 60
QY 61 QIMDVDEKNOVLTNIMLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120
DB 61 QIMDVDEKNOVLTNIMLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120
QY 121 RFDAFTHTNVLVNSGHCQYLPPIGIFKSSCYIDVRWPFDDVQHCCKLFGSWSYGGWSLDL 180
DB 121 RFDAFTHTNVLVNSGHCQYLPPIGIFKSSCYIDVRWPFDDVQHCCKLFGSWSYGGWSLDL 180
QY 181 QMQEADISGYIPNGEWDLVGIPIGKRSEFYECCKEYPDVTFTVTRRRTLYYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGIPIGKRSEFYECCKEYPDVTFTVTRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALALLVFLLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVIVLYQHHDDPGGKMPKTRVILLNCAWFLMRKRPGEKVRPACQHK 360
DB 301 MIIVGLSVVTVIVLYQHHDDPGGKMPKTRVILLNCAWFLMRKRPGEKVRPACQHK 360
QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
DB 361 QRCCLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
QY 421 LHGGQPEGDPDLAKILEEVRYIANFRQCDESAVCSWKFAACVVDRLCLMAFSVFTI 480
DB 421 LHGGQPEGDPDLAKILEEVRYIANFRQCDESAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 5

US-09-217-345-8
; Sequence 8, Application US/09217345
; Patent No. 6303753

GENERAL INFORMATION:

;; APPLICANT: Elliot, Kathryn J.
;; APPLICANT: Ellis, Steven B.
;; APPLICANT: Harpold, Michael M.
;; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
;; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:

ADDRESSEE: Heller Ehrman White & McLaughlin
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA: US/09/217,345
FILING DATE: 21-DEC-98
PRIOR APPLICATION NUMBER: US 08/467,574
FILING DATE: 05-JUN-95
PRIOR APPLICATION DATA:
FILING DATE: 05-JUN-95
APPLICATION NUMBER: US 08/466,589,
FILING DATE: 05-JUN-95
PRIOR APPLICATION DATA:
FILING DATE: 08-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9949B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-450-8400
TELEFAX: 619-587-5360
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 502 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-217-345-8

Query Match 99.8%; Score 2698; DB 4; Length 502;
Best Local Similarity 99.8%; Pred. No. 1.5e-273;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAALASLLHVSILQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
DB 1 MRCSPGGVWLAALASLLHVSILQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
QY 61 QIMDVDEKNOVLTNNIWLQSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120
DB 61 QIMDVDEKNOVLTNNIWLQSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120
QY 121 RPDATHNVLNSSGHCQVLPPIGFKSSCYIDVRWPFDDVQHCKLKFSGWSYGSWLSL 180
DB 121 RPDATHNVLNSSGHCQVLPPIGFKSSCYIDVRWPFDDVQHCKLKFSGWSYGSWLSL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGRSRFECCKEPPDVFTVTMRRRTLYYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGIPGRSRFECCKEPPDVFTVTMRRRTLYYGLNLLIP 240
QY 241 CVLISALALVFLLPADSGEKISLIGITVLLSLTFFMLLVAEIMPATSDSVPLIAQYFAS 300
DB 241 CVLISALALVFLLPADSGEKISLIGITVLLSLTFFMLLVAEIMPATSDSVPLIAQYFAS 300
QY 301 MIIIVGLSVVTVIVLQYHHHDPDGGKMPKWRTRVILLNCAWFLRMKRGEDKVRPACQHK 360
DB 301 MIIIVGLSVVTVIVLQYHHHDPDGGKMPKWRTRVILLNCAWFLRMKRGEDKVRPACQHK 360
QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVVCGRMACSPTHDHL 420
DB 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVVCGRMACSPTHDHL 420
QY 421 LHGQPPGPDPAKILEEVRYIANRRCODESEAVCSEWKFACVVDRLCLMAFVSFTI 480

DB 421 LHGQPPGPDPAKILEEVRYIANRRCODESEAVCSEWKFACVVDRLCLMAFVSFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 6
US-08-487-596-12
Sequence 12, Application US/08487596
Patent No. 6440681
GENERAL INFORMATION:
APPLICANT: Elliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
ANTAGONISTS FOR HUMAN NEURONAL
TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,596
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US94/02447
FILING DATE: 08-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,503
FILING DATE: 08-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
FILING DATE: 30-NOV-1992
APPLICATION NUMBER: US 07/938,154
FILING DATE: 03-APR-1990
APPLICATION NUMBER: US 07/504,455
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9951
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 502 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-487-596-12

Query Match 99.8%; Score 2698; DB 4; Length 502;
Best Local Similarity 99.8%; Pred. No. 1.5e-273;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAALASLLHVSILQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
DB 1 MRCSPGGVWLAALASLLHVSILQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSL 60

Qy	61	QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPCVKTVRPPDGOIWKPDILLYNSADE	120
Db	61	QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPCVKTVRPPDGOIWKPDILLYNSADE	120
Qy	121	RFDATFHTNVLVNSSGHCQOYLPPGIFKSSCYIDVRWFPEVDQCHLKFQSWSYGWSLDL	180
Db	121	RFDATFHTNVLVNSSGHCQOYLPPGIFKSSCYIDVRWFPEVDQCHLKFQSWSYGWSLDL	180
Qy	181	QMQRADISGYIPNGSBDLVGIPGKSERSEFYECKEPYPDVTFTVTRRRRTLYYGLNLLIP	240
Db	181	QMQRADISGYIPNGSBDLVGIPGKSERSEFYECKEPYPDVTFTVTRRRRTLYYGLNLLIP	240
Qy	241	CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST	300
Db	241	CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST	300
Qy	301	MIIVGLSVVTVTVIQLQYHHHPDGGCKMPKWTREVILLNCWAFELMKRCGEDKVRPACQHK	360
Db	301	MIIVGLSVVTVTVIQLQYHHHPDGGCKMPKWTREVILLNCWAFELMKRCGEDKVRPACQHK	360
Qy	361	QRRCSLASVENSASAVAPPASNGNLLIYIGFRGLDGVHCVPTPDGSGVCGRMACSPTHDEHL	420
Db	361	QRRCSLASVENSASAVAPPASNGNLLIYIGFRGLDGVHCVPTPDGSGVCGRMACSPTHDEHL	420
Qy	421	LHGQPPPEGDDPLAKILBEVRYIANRFRQDESEAVCSSEWKFAACVVDRLCLMAFSVFTI	480
Db	421	LHGQPPPEGDDPLAKILBEVRYIANRFRQDESEAVCSSEWKFAACVVDRLCLMAFSVFTI	480
Qy	481	ICTIGILMSAPNFVEAVSKDFA	502
Db	481	ICTIGILMSAPNFVEAVSKDFA	502

RESULT 7
 US-08-278-635B-7
 ; Sequence 7, Application US/08278635B
 ; Patent No. 5683912
 ; GENERAL INFORMATION:
 ; APPLICANT: ELGOYHEN, ANA BELEN
 ; APPLICANT: JOHNSON, DAVID S.
 ; APPLICANT: BOULTER, JAMES R.
 ; APPLICANT: HEINEMANN, STEPHEN F.
 ; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
 ; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GRAY CARY WARE & FREIDENRICH
 ; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
 ; CITY: SAN DIEGO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 92121
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/278,635B
 ; FILING DATE: 21-JUL-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: REITER, STEPHEN E.
 ; REGISTRATION NUMBER: 31,192
 ; REFERENCE/DOCKET NUMBER: P41 9771
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-677-1409
 ; TELEFAX: 619-677-1465
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 502 amino acids
 ; TYPE: amino acid

```
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-278-635B-7

Query Match          94.0%; Score 2540; DB 1; Length 502;
Best Local Similarity 93.6%; Pred. No. 5.2e-257;
Matches 465; Conservative 18; Mismatches 14; Indels 0; Gaps 0;

Qy      6 GGWLAALASLLHVSLSQGFBQRKLYKELVKNYNPLRPVANDSQPLTVYFSLSLQLIMDV 65
       |||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db      6 GGIWLALAAALLHVSLSQGFRRRLYKELVKNYNPLRPVANDSQPLTVYFSLSLQLIMDV 65
       |||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

Qy     66 DEKNQVLTTNIMLQNSWDTHYLQMNVSYPGVKYTRFPDGGQIWKDPIDILLYNSADERPDAT 125
       |||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db     66 DEKNQVLTTNIMLQNSWDTHYLQMNVSYPGVKYNRFPDGGQIWKDPIDILLYNSADERPDAT 125
       |||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

Qy    126 FHTNLVNSSGHCQYLPPGIFKSSSCVIDVRWFPPDVQHCKLKFGSWSYGGSLLDLQMGEA 185
       |||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db    126 FHTNLVNASHCQVLPPIFKSSCYIDVRWFPPDVQQCKLKFGSWSYGGSLLDLQMGEA 185
       |||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

Qy    186 DISGYIPNGEWDLVGIPGRSRFRFYECCKEPYDPVTFTVMRRTLYYGLNLLIPCVALIS 245
       |||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db    186 DISSYIPNGEWDLMGIPGRNEKFYECCKEPYDPVTYTVTMRRTLYYGLNLLIPCVALIS 245
       |||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

Qy    246 ALALLVFLLPADSGEKISLGITVLLSLTTFMILLVAEIMPATSDDSVPLIAQYFASTMIIVG 305
       |||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db    246 ALALLVFLLPADSGEKISLGITVLLSLTVMILLVAEIMPATSDDSVPLIAQYFASTMIIVG 305
       |||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

Qy    306 LSWVVTVIVLOVHHHDPPDGKKMPKWTRVILLNWCAFLRMKRPGEDKVVPACOHKRPQS 365
       |||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db    306 LSWVVTVIVLRVHHHDPPDGKKMPKWIRIILLNWCAFLRMKRPGEDKVVPACOHKRPQS 365
       |||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

Qy    366 LASVMSAVAPPASNGLLIYIGFRLGDGVCHVCTPTPDSGVVCGRMACSPTHDEHLHGQG 425
       |||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db    366 LASVELSAGAGPTSNGLLIYIGFRLGSMHCAPTPDSGVVCGRMACSPTHDEHLMHGHAH 425
       |||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

Qy    426 PPEGDPDLAKILLEEVRYIANRPRCODESEAWKFAACVVDRLCLMAFSVFTIICTIG 485
       |||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db    426 PSDGDPDLAKILLEEVRYIANRPRCODESEVICSEWKFAACVVDRLCLMAFSVFTIICTIG 485
       |||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

Qy    486 ILSAPNFVEAVSKDPA 502
       |||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db    486 ILSAPNFVEAVSKDPA 502
       |||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

RESULT 8
US-08-464-258B-7
; Sequence 7, Application US/08464258B
; Patent No. 6013766
; GENERAL INFORMATION:
; APPLICANT: ELGOVHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOUTLER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY CARY WARE & FREIDENRICH LLP
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,258B
; FILING DATE: 06/05/95
; CLASSIFICATION: 530
```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/278,635
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9989
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 502 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-464-2588-7

Query Match 94.0%; Score 2540; DB 3; Length 502;
Best Local Similarity 93.6%; Pred. No. 5.2e-257;
Matches 465; Conservative 18; Mismatches 14; Indels 0; Gaps 0;

QY 6 GGWLALAAALLHVSLOGEFORKLYKELVKYNPLERPVANDSOPLTIVYFSLSLQIMDV 65
DB 6 GGIWLAALAAALLHVSLOGEFORKLYKELVKYNPLERPVANDSOPLTIVYFSLSLQIMDV 65
QY 66 DEKNQVLTNIWLQMSWTDHYLQNMVSEYPGVKTVRPPDGOIKWPKDILLVNSADERFDAT 125
DB 66 DEKNQVLTNIWLQMSWTDHYLQNMVSEYPGVKTVRPPDGOIKWPKDILLVNSADERFDAT 125
QY 126 FHTNVLNVSNGHCQYLPPGIFKSSCYIDVRWFPDVOCKLKFGSWSGWMSLDLQMOEA 185
DB 126 FHTNVLNVSNGHCQYLPPGIFKSSCYIDVRWFPDVOCKLKFGSWSGWMSLDLQMOEA 185
QY 186 DISYIPNGEWDLVGIPGKRSEYFECCKEPYDPVTVTVMRRRTLYGLNLLIPCVLIS 245
DB 186 DISYIPNGEWDLVGIPGKRSEYFECCKEPYDPVTVTVMRRRTLYGLNLLIPCVLIS 245
QY 186 DISSYIPNGEWDLVGIPGKRSEYFECCKEPYDPVTVTVMRRRTLYGLNLLIPCVLIS 245
DB 186 DISSYIPNGEWDLVGIPGKRSEYFECCKEPYDPVTVTVMRRRTLYGLNLLIPCVLIS 245
QY 246 ALALLVFLPADSGEKISLGTIVLLSLTTFMLVAEIMPATSDSVPLIAQYFASTMIIVG 305
DB 246 ALALLVFLPADSGEKISLGTIVLLSLTTFMLVAEIMPATSDSVPLIAQYFASTMIIVG 305
QY 306 LSVVVTIVLYHHHPDGGKMPKWTIRVILLNWCWFLMKRPGEDKVRPACQHKQRRC 365
DB 306 LSVVVTIVLYHHHPDGGKMPKWTIRVILLNWCWFLMKRPGEDKVRPACQHKQRRC 365
QY 366 LASVMSAVAPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTDHEHLHGQ 425
DB 366 LASVMSAVAPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTDHEHLHGQ 425
QY 426 PPGDDPLAKILEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTIICIG 485
DB 426 PPGDDPLAKILEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTIICIG 485
QY 486 ILMGAPNFVEAVSKDFA 502
DB 486 ILMGAPNFVEAVSKDFA 502

RESULT 9
US-08-471-961-7
Sequence 7, Application US/08471961
Patent No. 6100046
GENERAL INFORMATION:
APPLICANT: ELGOYHEN, ANA BELEN
APPLICANT: JOHNSON, DAVID S.
APPLICANT: BOULTER, JAMES R.
APPLICANT: HEINEMANN, STEPHEN F.
TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAY CARY WARE & FREIDENRICH

STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,961
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,635
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9771
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 502 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-961-7

Query Match 94.0%; Score 2540; DB 3; Length 502;
Best Local Similarity 93.6%; Pred. No. 5.2e-257;
Matches 465; Conservative 18; Mismatches 14; Indels 0; Gaps 0;

QY 6 GGWLALAAALLHVSLOGEFORKLYKELVKYNPLERPVANDSOPLTIVYFSLSLQIMDV 65
DB 6 GGIWLAALAAALLHVSLOGEFORKLYKELVKYNPLERPVANDSOPLTIVYFSLSLQIMDV 65
QY 66 DEKNQVLTNIWLQMSWTDHYLQNMVSEYPGVKTVRPPDGOIKWPKDILLVNSADERFDAT 125
DB 66 DEKNQVLTNIWLQMSWTDHYLQNMVSEYPGVKTVRPPDGOIKWPKDILLVNSADERFDAT 125
QY 126 FHTNVLNVSNGHCQYLPPGIFKSSCYIDVRWFPDVOCKLKFGSWSGWMSLDLQMOEA 185
DB 126 FHTNVLNVSNGHCQYLPPGIFKSSCYIDVRWFPDVOCKLKFGSWSGWMSLDLQMOEA 185
QY 186 DISYIPNGEWDLVGIPGKRSEYFECCKEPYDPVTVTVMRRRTLYGLNLLIPCVLIS 245
DB 186 DISYIPNGEWDLVGIPGKRSEYFECCKEPYDPVTVTVMRRRTLYGLNLLIPCVLIS 245
QY 246 ALALLVFLPADSGEKISLGTIVLLSLTTFMLVAEIMPATSDSVPLIAQYFASTMIIVG 305
DB 246 ALALLVFLPADSGEKISLGTIVLLSLTTFMLVAEIMPATSDSVPLIAQYFASTMIIVG 305
QY 306 LSVVVTIVLYHHHPDGGKMPKWTIRVILLNWCWFLMKRPGEDKVRPACQHKQRRC 365
DB 306 LSVVVTIVLYHHHPDGGKMPKWTIRVILLNWCWFLMKRPGEDKVRPACQHKQRRC 365
QY 366 LASVMSAVAPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTDHEHLHGQ 425
DB 366 LASVMSAVAPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTDHEHLHGQ 425
QY 426 PPGDDPLAKILEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTIICIG 485
DB 426 PPGDDPLAKILEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTIICIG 485
QY 486 ILMGAPNFVEAVSKDFA 502
DB 486 ILMGAPNFVEAVSKDFA 502

Db	375	SLKNTMNVLPQHQPNSGNMIY-SYHTWENPCCPNQNDLGSKGKITCPLSDNHHVQKK	433
Qy	425	OPPEGDPDLAKILEVRVIANRFRQDESEAVCSWEKFAACVVDRCLCMAPSVFTIICI	484
Db	434	ALMDTIPVIVKILBEVOFIAMRFKQDEGEICSEWKFAAAVIDRLCLVAFLFALICTF	493
Qy	485	GILSAPNFVEAVSKDF 501	
Db	494	TILSAPNFIEAVSKDF 510	
RESULT 11			
US-08-464-258B-8			
; Sequence 8, Application US/08464258B			
; Patent No. 6013766			
; GENERAL INFORMATION:			
; APPLICANT: ELGOYHEN, ANA BELEN			
; APPLICANT: JOHNSON, DAVID S.			
; APPLICANT: BOULTER, JAMES R.			
; APPLICANT: HEINEMANN, STEPHEN F.			
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL			
; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR			
; NUMBER OF SEQUENCES: 8			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: GRAY CARY WARE & FREIDENRICH LLP			
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600			
; CITY: SAN DIEGO			
; STATE: CALIFORNIA			
; COUNTRY: USA			
; ZIP: 92121			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patentin Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/464.258B			
; FILING DATE: 06/05/95			
; CLASSIFICATION: 530			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 08/278,635			
; FILING DATE: 21-JUL-1994			
; ATTORNEY/AGENT INFORMATION:			
; NAME: REITER, STEPHEN E.			
; REGISTRATION NUMBER: 31,192			
; REFERENCE/DOCKET NUMBER: P41 9989			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 619-677-1409			
; TELEFAX: 619-677-1465			
; INFORMATION FOR SEQ ID NO: 8:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 511 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
US-08-278-635B-8			
Query Match 67.2%; Score 1816.5; DB 1; Length 511;			
Best Local Similarity 68.8%; Pred. No. 2.6e-181;			
Matches 342; Conservative 56; Mismatches 94; Indels 5; Gaps 4;			
Qy	8	VWLALAASLLHVSLOGEFORKLYKELVKYNPLRPVANDSQPLTVYFSLSLLQIMDVDE	67
Db	16	LWASLFSLFPKVSQQGESQRRLYDRLNRNLPRPVANDSQPIVWELQLSLLQIIDVDE	75
Qy	68	KNOVLTTNIWLQMSWTDDHYLQMNVSYPGVKTRVPDGIWKPKDILLYNSADERFDATFH	127
Db	76	KNOVLITNAWLQMYVDIYLSWDQYEPGVQNLRFPDSQIWVPDILLYNSADERFDATFH	135
Qy	128	TNVVNSSGHCOYLLPGCIFKSSCYIDVRPFPPDVQHCCLKFGWSYSGWSDLQMQRADI	187
Db	136	TNVLVNYSQCOYIPGILKSTCYIDVRWFPPDVQKCCLKFGSWTHSGWLDLQMLEADI	195
Qy	188	SGYIPNGEWDVGIPGKRSEFYECCKEYPDVTFTVMRRRTLYYGLNLLIPCVALISAL	247
Db	196	SNYSISNGEWDVGVPGRNELYYECKEYPDVTYTIMRRRTLYYGLNLLIPCVALISGL	255
Qy	248	ALLVFLPADSGEKISGITVLSLTFFMLLVAEIMPATSDSPVLIQAQYFASIMVIGLS	307
Db	256	ALLVFLPADSGEKISLGITVLSLTTFVFMLLVAEIMPATSDSPVLIQAQYFASIMVIGLS	315
Qy	308	VVTVTLVLOVHHDDPGGKMPKTRVILLNWCAWFLRMKPGBDKVRP-AQCHK--QRRK	364
Db	316	VVTVTLVLOVHHDDPGAGKMPRVIRVILLNWCAWFLRMKPGEN-IKPLSCKYSYPKHP	374
Qy	365	SLASVEMSAAVAPPASNGLLYIGFRGLDGVCVPTPDGSGVCGMACSPTHDEHLHG	424

QY 188 SGVIPNGEWDLVGPGRSERFYECCKEKPYDPVDTFTVMRRRTLYYGLNLLIPCVLISAL 247
 DB 196 SNYISNGEWDLVGPGRNELNYECCKEKPYDPVDTFTVMRRRTLYYGLNLLIPCVLISGL 255
 QY 248 ALLVFLPADSGEKISLIGITVLLSLTFMMLVAEIMPATSDSVPLIAQYFASIMVIGLS 307
 DB 256 ALLVFLPADSGEKISLIGITVLLSLTFMMLVAEIMPATSDSVPLIAQYFASIMVIGLS 315
 QY 308 VVTVIVLVQHHHDPDGGKMPKTRVILLNWCWFLRMKRPGEKVRP-ACQHK--QRRK 364
 DB 316 VVTVIVLVQHHHDPDGGKMPKTRVILLNWCWFLRMKRPGEKVRP-ACQHK--QRRK 374
 QY 365 SLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTDPSGVVCGRMACSPTHDEHLLHGG 424
 DB 375 SLKNTMNVLPQHPSNGNMIY-SYHTMENPCCPNNDLGSKSGKITCPLSEDNEHVQKK 433
 QY 425 QPPEGDPDLAKILEEVRYIANRRCODESEAVCSEWKFACVVDRLCLMAFVSFTIICTI 484
 DB 434 ALMDTIPVIVKILEEVQFIAMRFRKQDEGEICSEWKFACVVDRLCLMAFVSFTIICTF 493
 QY 485 GILMSAPNFIEAVSKDF 501
 DB 494 TILMSAPNFIEAVSKDF 510

RESULT 12
 US-08-471-961-8
 ; Sequence 8, Application US/08471961
 ; Patent No. 6100046
 ; GENERAL INFORMATION:
 ; APPLICANT: ELGOYHEN, ANA BELEN
 ; APPLICANT: JOHNSON, DAVID S.
 ; APPLICANT: BOULTER, JAMES R.
 ; APPLICANT: HEINEMANN, STEPHEN F.
 ; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
 ; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GRAY CARY WARE & FREIDENRICH
 ; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
 ; CITY: SAN DIEGO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 92121
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/471,961
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/278,635
 ; FILING DATE: 21-JUL-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: REITER, STEPHEN E.
 ; REGISTRATION NUMBER: 31,192
 ; REFERENCE/DOCKET NUMBER: P41 9771
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-677-1409
 ; TELEFAX: 619-677-1465
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 511 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-471-961-8
 Query Match 67.2%; Score 1816.5; DB 3; Length 511;
 Best Local Similarity 68.8%; Pred. No. 2.6e-181;

Matches 342; Conservative 56; Mismatches 94; Indels 5; Gaps 4;
 QY 8 VWLALAAASLLHVSLSQGEFQRLKYLKVNPNPLRPVANDSQPLTVFSLSLQIQIMVDVE 67
 DB 16 LWASLFLSFFKVSQGESQRLYDLRLNRYNRLRPVNDQSPVIVLQSLQIIVDVE 75
 QY 68 KNOVLTNNIWLQMSWTDHYLQWNVSEYGPVKTVRFPDQGIWKPDILLVNSADERPDATFH 127
 DB 76 KNOVLTNNIWLQMSWTDHYLQWNVSEYGPVKTVRFPDQGIWKPDILLVNSADERPDATFH 135
 QY 128 TNVLVNSSGHCOYLPGRIFKSSCYIDVRWPPFDVQHKCLKFSGWSYSGWSDLOMQEADI 187
 DB 136 TNVLVNSSGHCOYLPGRIFKSSCYIDVRWPPFDVQHKCLKFSGWTHSGWLDLOQLEADI 195
 QY 188 SGVIPNGEWDLVGPGRSERFYECCKEKPYDPVDTFTVMRRRTLYYGLNLLIPCVLISAL 247
 DB 196 SNYISNGEWDLVGPGRNELNYECCKEKPYDPVDTFTVMRRRTLYYGLNLLIPCVLISGL 255
 QY 248 ALLVFLPADSGEKISLIGITVLLSLTFMMLVAEIMPATSDSVPLIAQYFASIMVIGLS 307
 DB 256 ALLVFLPADSGEKISLIGITVLLSLTFMMLVAEIMPATSDSVPLIAQYFASIMVIGLS 315
 QY 308 VVTVIVLVQHHHDPDGGKMPKTRVILLNWCWFLRMKRPGEKVRP-ACQHK--QRRK 364
 DB 316 VVTVIVLVQHHHDPDGGKMPKTRVILLNWCWFLRMKRPGEKVRP-ACQHK--QRRK 374
 QY 365 SLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTDPSGVVCGRMACSPTHDEHLLHGG 424
 DB 375 SLKNTMNVLPQHPSNGNMIY-SYHTMENPCCPNNDLGSKSGKITCPLSEDNEHVQKK 433
 QY 425 QPPEGDPDLAKILEEVRYIANRRCODESEAVCSEWKFACVVDRLCLMAFVSFTIICTI 484
 DB 434 ALMDTIPVIVKILEEVQFIAMRFRKQDEGEICSEWKFACVVDRLCLMAFVSFTIICTF 493
 QY 485 GILMSAPNFIEAVSKDF 501
 DB 494 TILMSAPNFIEAVSKDF 510
 RESULT 13
 US-08-496-855A-2
 ; Sequence 2, Application US/08496855A
 ; Patent No. 5801232
 ; GENERAL INFORMATION:
 ; APPLICANT: Elliot, Kathryn J.
 ; APPLICANT: Ellis, Steven B.
 ; APPLICANT: Harpold, Michael M.
 ; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
 ; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & McClain
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: CA
 ; COUNTRY: U.S.A.
 ; ZIP: 92101-2926
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/496,855A
 ; FILING DATE: 20-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/149,503
 ; FILING DATE: 08-NOV-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/028,031
 ; FILING DATE: 08-MAR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seidman, Stephanie

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/487,596
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US94/02447
FILING DATE: 08-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,503
FILING DATE: 08-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,154
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/504,455
FILING DATE: 03-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9951
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 529 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-487-596-2

Query Match	35.0%;	Score	945;	DB	4;	Length	529;
Best Local Similarity	39.8%;	Pred. No.	4.1e-90;				
Matches	200;	Conservative	78;	Mismatches	160;	Indels	64;
Gaps	9						

Qy	24	EFORKLKELVKNVPLRPVANDSQPLTVYVFSLSLQIMDVDEKNQVLTNNIWLQMSWT	83
Db	57	ETEDRLFKHLPGRGNRWARPVNTSDVVVIFRFGUSIAQLIDVDKQNMMTNNVWLKQWS	116
Qy	84	DHYLQWNVSYPGVKTVFRFDGQWKPKDILLYNSADERFDATFHTNVLVNSSGHCQYLPP	143
Db	117	DYKLWNVPADGNITSLRVSEMIWIPIDIVLYNNADGEFAVTHMTKAHLFSTGTVHWVVP	176
Qy	144	GIFKSSCYIDVRWFPFVQHQCKLKFSGNSYGGWSLDLQMQE--ADISGYINGEWDLVGI	201
Db	177	AIYKSSCSIDVTFPPFQOQCKMKFGSWTDKAKIDLEQMEQTVDLKDYWESSGEAI	236
Qy	202	PKGRSEFFYECCKEPYDNTFTVTMRRTLYYGNLNIIPCVLISALALLVLLPADSCEK	261
Db	237	TGYNSKKYDCCAEIYPDVTYAFVIRKLPFYTTINLIIPCLLISCLTVLVFLPSPDCEK	296
Qy	262	ISLGITVLLSTTFMLIVAEIMPATSDSVPLIAQYFASMTIIVGLSVVTVTVIVLQYHH	321
Db	297	ITLCISVLLSLTVFLLLITETIIPSTSLVPLIGEYLLFTMIFVLSIVITVFLNVHRS	356
Qy	322	PDGKMPKPTRVILLNKCWFLMRKRGEDKVRPACQHKORRCSLASVEMSAVAPPASN	381
Db	357	PSHTHPHWVRGALLGCVPRLMMNRP-----PPPVVL	389
Qy	382	GNLLXI-----GFRGLDG-----VHCVPPTDSGVWGRMA-----CSPTHDEHLHGG	424
Db	390	CHPLRLKLSPSYHWNLSNVDAERREVVVEEDRWACAGHVAPSVGTLCSHGH-----LHSG	445
Qy	425	QP-----PEGD-----PDLAKILEBVRVIANRFRQDSEAVCSBWKFAACVVDRLCL	472

Db 446 ASQPKAELLQEGELLSPHQKALEGVHYIADHLRSEDADSSVKEDWKYVAMVIDRIFL 505

QY 473 MAFSVFTIITIGILMSAPNFV 494

Db 506 WLFIIVFLGTIGLFL--PPFL 525

RESULT 15

US-08-278-635B-4
 ; Sequence 4, Application US/08278635B
 ; Patent No. 568912
 ; GENERAL INFORMATION:
 ; APPLICANT: ELGOYHEN, ANA BELEN
 ; APPLICANT: JOHNSON, DAVID S.
 ; APPLICANT: BOULTER, JAMES R.
 ; APPLICANT: HEINEMANN, STEPHEN F.
 ; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
 ; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GRAY CARY WARE & FREIDENRICH
 ; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
 ; CITY: SAN DIEGO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 92121
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/278,635B
 ; FILING DATE: 21-JUL-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: REITER, STEPHEN E.
 ; REGISTRATION NUMBER: 31,192
 ; REFERENCE/DOCKET NUMBER: P41 9771
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-677-1409
 ; TELEFAX: 619-677-1465
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 510 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-278-635B-4

Query Match 34.9%; Score 943; DB 1; Length 510;
 Best Local Similarity 39.0%; Pred. No. 6.2e-90;
 Matches 201; Conservative 83; Mismatches 178; Indels 54; Gaps 9;
 QY 8 VW--LALAASLLHSLQGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLOIMDV 65
 Db 16 LWCLLLVPAVLTOQGSHTAEDRLFKHLFGGYNRWARPVNTSDVIVRFGLSIAQLIDV 75
 QY 66 DEKNQVLTINILQMSWDHYLOWNVSEYPGVKTVPDPGQIWKPDILLYNSADERFDAT 125
 Db 76 DEKNQMTTNNVLKQENDYNVRDPAEFGNVTSIRVPSEMIWIPDIVLYNNADGEFATV 135
 QY 126 FHTNVLVNSGHCOYLPPIGFKSSCYIDVRFPDQVQHKLKFGSWSYGGWSLDLQMOE- 184
 Db 136 HMTKAHLFFGTGVHVPVPAIYKSSCIDVTFEPFDQOQCKMKFGSWTYDKAKIDLEQMER 195
 QY 185 -ADISGYPNGENDLVGPGRSERFYECCKEYDPDVTFTVMRRRTLYYGLNLLIPCVL 243
 Db 196 TVDLKDYWESGEWAINATGYNSKKYDCCAEIYPDVTYTVFVIRRLPLFYTNLIIPCL 255
 QY 244 ISALALVFLPADSGEKISLIGITVLLSLTTFMLIVAEIMPATSDSVPLIAQYFASMTII 303
 Db 256 ISCLTVLVFVLPSECGEKITLCISVLSLTVFLLLITELIIPSTSLVPIGLEYLLFTWIF 315

QY 304 VGLSVVVTVIYVLYHHDDPDGGRMPKWTRVILLNWCAMFLRMKRP-----GEDKVRPA 356
 Db 316 VTLISIVITVFLVNVHRSPTSTHNNPNVVRVALLGRVPRWLMNRPPLPMELHGSPLDKLS 375
 QY 357 CQHKQRCRLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDS--GVVCGRMACSP 414
 Db 376 PSYHWTNMDAGEREETEEEEEDENICV-----CAGLPDSSMGVLYG----- 419
 QY 415 THDEHLLHGG-----QPPEG-----DPDLAKILEEVRYTIANRFRCODESEAVCS 458
 Db 420 -----HGGHLHRAPEPETTPSQASEILLSPQIKALEGVHYIADHLRSEDADSSVKE 472
 QY 459 EWKFAACVVDRLCLMAFSVFTIITIGILMSAPNFV 494
 Db 473 DWKYVAMVDRIFLWLFIIVFLGTIGLFL--PPFL 506

Search completed: June 20, 2003, 19:01:50
 Job time : 29 secs

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OM protein - protein search, using sw model

Run on: June 20, 2003, 19:10:22 ; Search time 27 Seconds
(without alignments)
547.048 Million cell updates/sec

Title: US-09-954-936-2
Perfect score: 502
Sequence: 1 MRCSPGGVWLAALASLLHVS.....TIGILMSAPNFVEAVSKDFA 502

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 6

Total number of hits satisfying chosen parameters: 766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	502	100.0	502	4	US-08-771-737-2
2	401	79.9	502	2	US-08-466-589-8
3	401	79.9	502	2	US-08-700-636-8
4	401	79.9	502	3	US-08-467-574-8
5	401	79.9	502	4	US-09-217-345-8
6	401	79.9	502	4	US-08-487-596-12
7	62	12.4	502	1	US-08-278-635B-7
8	62	12.4	502	3	US-08-464-258B-7
9	62	12.4	502	3	US-08-471-961-7
10	27	5.4	511	1	US-08-278-635B-8
11	27	5.4	511	3	US-08-464-258B-8
12	27	5.4	511	3	US-08-471-961-8
13	10	2.0	479	1	US-08-278-635B-2
14	10	2.0	479	3	US-08-464-258B-2
15	10	2.0	479	3	US-08-471-961-2
16	8	1.6	141	1	US-07-695-564-5
17	8	1.6	141	1	US-08-241-387-5
18	8	1.6	149	1	US-07-695-564-7
19	8	1.6	149	1	US-08-241-387-7
20	7	1.4	29	4	US-09-227-357-184
21	7	1.4	37	4	US-09-227-357-399
22	7	1.4	73	2	US-08-997-080-141
23	7	1.4	73	2	US-08-997-362-141
24	7	1.4	73	4	US-09-095-855-141
25	7	1.4	73	4	US-09-324-542-141
26	7	1.4	73	4	US-09-205-426-141
27	7	1.4	157	2	US-08-164-292B-4

28	7	1.4	157	3	US-08-845-623-4	Sequence 4, Appli
29	7	1.4	157	3	US-08-815-927-4	Sequence 4, Appli
30	7	1.4	157	4	US-09-103-330-4	Sequence 4, Appli
31	7	1.4	157	4	US-09-435-242-4	Sequence 4, Appli
32	7	1.4	174	2	US-08-683-262B-45	Sequence 45, Appli
33	7	1.4	174	2	US-08-683-262B-48	Sequence 48, Appli
34	7	1.4	174	3	US-09-122-443-6	Sequence 6, Appli
35	7	1.4	174	4	US-09-361-707-45	Sequence 45, Appli
36	7	1.4	174	4	US-09-361-707-48	Sequence 48, Appli
37	7	1.4	183	4	US-09-615-192A-303	Sequence 303, App
38	7	1.4	261	4	US-09-134-001C-4966	Sequence 4966, Ap
39	7	1.4	268	4	US-09-383-586-14	Sequence 14, Appli
40	7	1.4	331	2	US-08-997-080-182	Sequence 182, App
41	7	1.4	331	2	US-08-997-362-182	Sequence 182, App
42	7	1.4	331	4	US-09-095-855-182	Sequence 182, App
43	7	1.4	331	4	US-09-324-542-182	Sequence 182, App
44	7	1.4	331	4	US-09-205-426-182	Sequence 182, App
45	7	1.4	352	4	US-09-576-160B-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-08-771-737-2
; Sequence 2, Application US/08771737
; Patent No. 6323000
; GENERAL INFORMATION:
; APPLICANT: Briggs, Clark A.
; APPLICANT: Gopalakrishnan, Murali
; APPLICANT: McKenna, David G.
; APPLICANT: Monteggia, Lisa M.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Sullivan, James P.
; APPLICANT: Touma, Edward
; APPLICANT: Abbott Laboratories
; TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE
; FILE REFERENCE: 6017.US.01
; CURRENT APPLICATION NUMBER: US/08/771,737
; CURRENT FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 502
; TYPE: PRT
; ORGANISM: homo sapien
US-08-771-737-2

Query Match 100.0%; Score 502; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRCSPGGVWLAALASLLHVS	LQGEFQRKLYKELVKNYNPLRPVANDSQPLTVYFSL	60
Db	1	MRCSPGGVWLAALASLLHVS	LQGEFQRKLYKELVKNYNPLRPVANDSQPLTVYFSL	60
Qy	61	QIMVDKRNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE	120	
Db	61	QIMVDKRNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE	120	
Qy	121	RFDAFTHNNVLSNGHCOYLPGGIFKSSCYDVRWFFPDVQHCKLKEGWSYGSW	180	
Db	121	RFDAFTHNNVLSNGHCOYLPGGIFKSSCYDVRWFFPDVQHCKLKEGWSYGSW	180	
Qy	181	QMQRADISGYIPNGEWDLVGIPGKRSEFYECCKEPEYPDVFTVTMRRTLYYGLNLLIP	240	
Db	181	QMQRADISGYIPNGEWDLVGIPGKRSEFYECCKEPEYPDVFTVTMRRTLYYGLNLLIP	240	
Qy	241	CVLISALALLVFLPADSGEKISLIGITVLLSLTTFMLLVABIMPATSDSVPLIAQYFAST	300	
Db	241	CVLISALALLVFLPADSGEKISLIGITVLLSLTTFMLLVABIMPATSDSVPLIAQYFAST	300	

QY 301 MIIVGLSVVTVIVLQYHHDDPGKMPKWKTRVILLNWCWFLMRKRPGEKVRPACQHK 360
 Db 301 MIIVGLSVVTVIVLQYHHDDPGKMPKWKTRVILLNWCWFLMRKRPGEKVRPACQHK 360
 QY 361 QRCCLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 Db 361 QRCCLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 QY 421 LHGGOPPEGDPDLAKILEEVRYIANRFRCODESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
 Db 421 LHGGOPPEGDPDLAKILEEVRYIANRFRCODESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 2

US-08-466-589-8
 ; Sequence 8, Application US/08466589
 ; Patent No. 5837489
 ; GENERAL INFORMATION:
 ; APPLICANT: Eliot, Kathryn J.
 ; APPLICANT: Ellis, Steven B.
 ; APPLICANT: Harpold, Michael M.
 ; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
 ; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & McClaim
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92101-2926
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/466,589
 ; FILING DATE: June 5, 1995
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/028,031
 ; FILING DATE: March 8, 1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seidman, Stephanie L
 ; REGISTRATION NUMBER: 33,779
 ; REFERENCE/DOCKET NUMBER: 6362-9950
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-238-0999
 ; TELEFAX: 619-238-0062
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 502 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-08-466-589-8

Query Match 79.9%; Score 401; DB 2; Length 502;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches: 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MRCSPGGWMLAASLLHVSLOQEFQKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
 Db 1 MRCSPGGWMLAASLLHVSLOQEFQKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
 QY .61 QIMDVEKNOVLTNIWLQMSWTDHYLQWNVSEYPGVKTRFPDGOIWKPDILLYNSADE 120

Db 61 QIMDVEKNOVLTNIWLQMSWTDHYLQWNVSEYPGVKTRFPDGOIWKPDILLYNSADE 120
 QY 121 RFDAFTHTNVLNVSNGHCOYLPGIFKSSCYIDVRWFFPDVQHCXKLFKFGWSYGSJDL 180
 Db 121 RFDAFTHTNVLNVSNGHCOYLPGIFKSSCYIDVRWFFPDVQHCXKLFKFGWSYGSJDL 180
 QY 181 QMGEADISGYIPNGEWDLVGIPGKRSEYFECCKEYEPDVTFTTMRRTLYYGLNLLIP 240
 Db 181 QMGEADISGYIPNGEWDLVGIPGKRSEYFECCKEYEPDVTFTTMRRTLYYGLNLLIP 240
 QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTFTMLLVABIMPATSDSVPLIAQYFAST 300
 Db 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTFTMLLVABIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVTVIVLQYHHDDPGKMPKWKTRVILLNWCWFLMRKRPGEKVRPACQHK 360
 Db 301 MIIVGLSVVTVIVLQYHHDDPGKMPKWKTRVILLNWCWFLMRKRPGEKVRPACQHK 360
 QY 361 QRCCLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 Db 361 QRCCLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 QY 421 LHGGOPPEGDPDLAKILEEVRYIANRFRCODESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
 Db 421 LHGGOPPEGDPDLAKILEEVRYIANRFRCODESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 3

US-08-700-636-8
 ; Sequence 8, Application US/08700636
 ; Patent No. 5910582
 ; GENERAL INFORMATION:
 ; APPLICANT: Eliot, Kathryn J.
 ; APPLICANT: Ellis, Steven B.
 ; APPLICANT: Harpold, Michael M.
 ; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
 ; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
 ; STREET: 444 South Flower Street, Suite 2000
 ; CITY: Los Angeles
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 90071
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/700,636
 ; FILING DATE: 16-JUL-1996
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/028,031
 ; FILING DATE: 08-MAR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Reiter, Stephen E.
 ; REGISTRATION NUMBER: 31,192
 ; REFERENCE/DOCKET NUMBER: P41 9368
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-546-4737
 ; TELEFAX: 619-546-9392
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 502 amino acids
 ; TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-700-636-8

Query Match 79.9%; Score 401; DB 2; Length 502;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MRCSPGGWALAAASLLHVSLOGEFORKLYKELVKNVPLRPVANDSQPLTVYFSL 60
Db 1 MRCSPGGWALAAASLLHVSLOGEFORKLYKELVKNVPLRPVANDSQPLTVYFSL 60
Qy 61 QIMDVDEKQVLTNTNWLQSWTDHYLQWNVSEYPGVKTVPDGOIWKPDILLYNSADE 120
Db 61 QIMDVDEKQVLTNTNWLQSWTDHYLQWNVSEYPGVKTVPDGOIWKPDILLYNSADE 120
Qy 121 RDATEFTNTNVLNVSNGHCQYLPFGIKSSCYIDVRWPFDDVQHCCKLFGSWSYGGWSL 180
Db 121 RDATEFTNTNVLNVSNGHCQYLPFGIKSSCYIDVRWPFDDVQHCCKLFGSWSYGGWSL 180
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Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRTLYYGLNLLIP 240
Qy 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
Qy 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
Qy 361 QRCCLASVEMSAVAPPPASNGNLLYIGFRLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
Db 361 QRCCLASVEMSAVAPPPASNGNLLYIGFRLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
Qy 421 LHGGQPPGDPDLAKILEEVRYIANFRQDESEAVCEWKFACVVDRLCLMAFSVFTI 480
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Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 4
US-08-467-574-8
Sequence 8, Application US/08467574
Patent No. 6022704

GENERAL INFORMATION:
APPLICANT: Elliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSES: Brown, Martin, Haller & McClaim
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-Seq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,574
FILING DATE: June 5, 1995
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: March 8, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9949
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 502 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-467-574-8

Query Match 79.9%; Score 401; DB 3; Length 502;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MRCSPGGWALAAASLLHVSLOGEFORKLYKELVKNVPLRPVANDSQPLTVYFSL 60
Db 1 MRCSPGGWALAAASLLHVSLOGEFORKLYKELVKNVPLRPVANDSQPLTVYFSL 60
Qy 61 QIMDVDEKQVLTNTNWLQSWTDHYLQWNVSEYPGVKTVPDGOIWKPDILLYNSADE 120
Db 61 QIMDVDEKQVLTNTNWLQSWTDHYLQWNVSEYPGVKTVPDGOIWKPDILLYNSADE 120
Qy 121 RDATEFTNTNVLNVSNGHCQYLPFGIKSSCYIDVRWPFDDVQHCCKLFGSWSYGGWSL 180
Db 121 RDATEFTNTNVLNVSNGHCQYLPFGIKSSCYIDVRWPFDDVQHCCKLFGSWSYGGWSL 180
Qy 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRTLYYGLNLLIP 240
Qy 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
Qy 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
Qy 361 QRCCLASVEMSAVAPPPASNGNLLYIGFRLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
Db 361 QRCCLASVEMSAVAPPPASNGNLLYIGFRLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
Qy 421 LHGGQPPGDPDLAKILEEVRYIANFRQDESEAVCEWKFACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPGDPDLAKILEEVRYIANFRQDESEAVCEWKFACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 5
US-09-217-345-8
Sequence 8, Application US/09217345
Patent No. 6303753

GENERAL INFORMATION:
APPLICANT: Elliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:

; ADDRESSEE: Heller Ehrman White & McAuliffe
 ; STREET: 4250 Executive Square, 7th Floor
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/217,345
 ; FILING DATE: 21-DEC-98
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/467,574
 ; FILING DATE: 05-JUN-95
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/466,589
 ; FILING DATE: 05-JUN-95
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/028,031
 ; FILING DATE: 08-MAR-93
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seidman, Stephanie L.
 ; REGISTRATION NUMBER: 33,779
 ; REFERENCE/DOCKET NUMBER: 24735-9949B
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-450-8400
 ; TELEFAX: 619-587-5360
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 502 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-09-217-345-8

Query Match 79.9%; Score 401; DB 4; Length 502;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAASLLHVSLSQGEFQRLKYLKVNPNPLRPVANDSOPLTVYFSL 60
 DB 1 MRCSPGGVWLAASLLHVSLSQGEFQRLKYLKVNPNPLRPVANDSOPLTVYFSL 60
 QY 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTFRFDCQIWKPDILLYNSADE 120
 DB 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTFRFDCQIWKPDILLYNSADE 120
 QY 121 REFATHTNVLNNSGHCQYLPPGIFKSSCYIDVRWPFDFVQHCKLKFGSWSYGGWSLDL 180
 DB 121 REFATHTNVLNNSGHCQYLPPGIFKSSCYIDVRWPFDFVQHCKLKFGSWSYGGWSLDL 180
 QY 181 QMGEADISGYPNGEWDLVGIPKRSRFEYCKEPPDVTFTVTMRRTLYYGLNLLIP 240
 DB 181 QMGEADISGYPNGEWDLVGIPKRSRFEYCKEPPDVTFTVTMRRTLYYGLNLLIP 240
 QY 241 CVLISALALVFLPADSGEKISLIGITVLLSLTFFMLLVAEIMPATSDSVPLIAQYFAST 300
 DB 241 CVLISALALVFLPADSGEKISLIGITVLLSLTFFMLLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVTVIVLQYHHHDPDGGKMPKTRVILLNWCAMFLRMKRPGEDKVRPAQCHK 360
 DB 301 MIIVGLSVVTVIVLQYHHHDPDGGKMPKTRVILLNWCAMFLRMKRPGEDKVRPAQCHK 360
 QY 361 QRCCLASVMSAVAPPPASNGNLLYIGFRGLDGVHCVPPTDPSGVGVCGRMACSTHDEHL 420
 DB 361 QRCCLASVMSAVAPPPASNGNLLYIGFRGLDGVHCVPPTDPSGVGVCGRMACSTHDEHL 420
 QY 421 LHGGQPEGPDIAKILEEVRYIANRRCQDESEAVCSWKFAACVVDRLCLMAFVSFTI 480

DB 421 LHGGQPEGPDIAKILEEVRYIANRRCQDESEAVCSWKFAACVVDRLCLMAFVSFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 DB 481 ICTIGILMSAPNFVEAVSKDFA 502
 RESULT 6
 US-08-487-596-12
 ; Sequence 12, Application US/08487596
 ; Patent No. 6440681
 ; GENERAL INFORMATION:
 ; APPLICANT: Elliot, Kathryn J.
 ; APPLICANT: Ellis, Steven B.
 ; APPLICANT: Harpold, Michael M.
 ; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
 ; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL
 ; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & McClain
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/487,596
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO US94/02447
 ; FILING DATE: 08-MAR-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/149,503
 ; FILING DATE: 08-NOV-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/028,031
 ; FILING DATE: 08-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/938,154
 ; FILING DATE: 30-NOV-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/504,455
 ; FILING DATE: 03-APR-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seidman, Stephanie L.
 ; REGISTRATION NUMBER: 33,779
 ; REFERENCE/DOCKET NUMBER: 6362-9951
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-238-0999
 ; TELEFAX: 619-238-0062
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 502 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-08-487-596-12

Query Match 79.9%; Score 401; DB 4; Length 502;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAASLLHVSLSQGEFQRLKYLKVNPNPLRPVANDSOPLTVYFSL 60
 DB 1 MRCSPGGVWLAASLLHVSLSQGEFQRLKYLKVNPNPLRPVANDSOPLTVYFSL 60

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QY 61 QIMDVDEKNOVLTNNIWLQSWTDHYLQNMVSEYGVKTVRFDGQIWKPDILLYNSADE 120
Db 61 QIMDVDEKNOVLTNNIWLQSWTDHYLQNMVSEYGVKTVRFDGQIWKPDILLYNSADE 120
QY 121 RFDATHTNNVNLSSGHCQYLPPGIPKSSCVIDVRWFFPDVQHCCKLFGWSYSGWSL 180
Db 121 RFDATHTNNVNLSSGHCQYLPPGIPKSSCVIDVRWFFPDVQHCCKLFGWSYSGWSL 180
QY 181 QMGEADISGYPNGEWDLVIGPKRSERFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIP 240
Db 181 QMGEADISGYPNGEWDLVIGPKRSERFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTTFMLLVABIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTTFMLLVABIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVTVLQVHHHDPDGGKMPKWTIRVILLNWCWFLRMKPGEDKVRPACQHK 360
Db 301 MIIVGLSVVTVTVLQVHHHDPDGGKMPKWTIRVILLNWCWFLRMKPGEDKVRPACQHK 360
QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPEGDPDLAKILEEVRYIANRFRQCODESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPEGDPDLAKILEEVRYIANRFRQCODESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNEVEAVSKDFA 502
Db 481 ICTIGILMSAPNEVEAVSKDFA 502

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RESULT 7
US-08-278-635B-7
; Sequence 7, Application US/08278635B
; Patent No. 5683912
; GENERAL INFORMATION:
; APPLICANT: ELGOVHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY CARY WARE & FREIDENRICH LLP
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/278,635B
; FILING DATE: 21-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: REITER, STEPHEN E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9771
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-278-635B-7
Query Match
Best Local Similarity 12.4%; Score 62; DB 1; Length 502;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 LYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMDVDEKNOVLTNNIWLQSWTDHYLQ 88
Db 29 LYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMDVDEKNOVLTNNIWLQSWTDHYLQ 88
QY 89 WN 90
Db 89 WN 90
RESULT 8
US-08-464-258B-7
; Sequence 7, Application US/08464258B
; Patent No. 6013766
; GENERAL INFORMATION:
; APPLICANT: ELGOVHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY CARY WARE & FREIDENRICH LLP
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,258B
; FILING DATE: 06/05/95
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/278,635
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: REITER, STEPHEN E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9989
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-464-258B-7
Query Match
Best Local Similarity 12.4%; Score 62; DB 3; Length 502;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 LYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMDVDEKNOVLTNNIWLQSWTDHYLQ 88
Db 29 LYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMDVDEKNOVLTNNIWLQSWTDHYLQ 88
QY 89 WN 90
Db 89 WN 90

```

Db 89 WN 90

RESULT 9
US-08-471-961-7
; Sequence 7, Application US/08471961
; Patent No. 6100046
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY CARY WARE & FREIDENRICH
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,961
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,635
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: REITER, STEPHEN E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9771
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-961-7

Query Match 12.4%; Score 62; DB 3; Length 502;
Best Local Similarity 100.0%; Pred. No. 1e-51;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 LYKELVKNYPLRPVANDSQPLTVFSLQLQIMDVDEKNOVLTTNIWLQMSWTDHYLQ 88
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Db 29 LYKELVKNYPLRPVANDSQPLTVFSLQLQIMDVDEKNOVLTTNIWLQMSWTDHYLQ 88
|||||

QY 89 WN 90
||
Db 89 WN 90

RESULT 10
US-08-278-635B-8
; Sequence 8, Application US/08278635B
; Patent No. 5683912
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAY CARY WARE & FREIDENRICH
STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,635B
FILING DATE: 21-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9771
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 511 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-278-635B-8

Query Match 5.4%; Score 27; DB 1; Length 511;
Best Local Similarity 100.0%; Pred. No. 7e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 LALLVFLLPADSGEKISLGITVLLSLT 273
|||||
Db 255 LALLVFLLPADSGEKISLGITVLLSLT 281
|||||

RESULT 11
US-08-464-258B-8
; Sequence 8, Application US/08464258B
; Patent No. 6013766
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY CARY WARE & FREIDENRICH LLP
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,258B
; FILING DATE: 06/05/95
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/278,635
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:

NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9989
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 511 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-464-258B-8

Query Match 5.4%; Score 27; DB 3; Length 511;
Best Local Similarity 100.0%; Pred. No. 7e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 LALLVLLPADSGEKISLIGITVLLSLT 273
|||
Db 255 LALLVLLPADSGEKISLIGITVLLSLT 281

RESULT 12
US-08-471-961-8
Sequence 8, Application US/08471961
Patent No. 6100046
GENERAL INFORMATION:
APPLICANT: ELGOYHEN, ANA BELEN
APPLICANT: JOHNSON, DAVID S.
APPLICANT: BOULTER, JAMES R.
APPLICANT: HEINEMANN, STEPHEN F.
TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAY CARY WARE & FREIDENRICH
STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,961
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,635
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9771
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 511 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-961-8

Query Match 5.4%; Score 27; DB 3; Length 511;
Best Local Similarity 100.0%; Pred. No. 7e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 LALLVLLPADSGEKISLIGITVLLSLT 273
|||
Db 255 LALLVLLPADSGEKISLIGITVLLSLT 281

RESULT 13
US-08-278-635B-2
Sequence 2, Application US/08278635B
Patent No. 5683912
GENERAL INFORMATION:
APPLICANT: ELGOYHEN, ANA BELEN
APPLICANT: JOHNSON, DAVID S.
APPLICANT: BOULTER, JAMES R.
APPLICANT: HEINEMANN, STEPHEN F.
TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAY CARY WARE & FREIDENRICH
STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,635B
FILING DATE: 21-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9771
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 479 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-278-635B-2

Query Match 2.0%; Score 10; DB 1; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 NLLIPCVLIS 245
|||
Db 243 NLLIPCVLIS 252

RESULT 14
US-08-464-258B-2
Sequence 2, Application US/08464258B
Patent No. 6013766
GENERAL INFORMATION:
APPLICANT: ELGOYHEN, ANA BELEN
APPLICANT: JOHNSON, DAVID S.
APPLICANT: BOULTER, JAMES R.
APPLICANT: HEINEMANN, STEPHEN F.
TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAY CARY WARE & FREIDENRICH LLP
STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
CITY: SAN DIEGO

STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,258B
FILING DATE: 06/05/95
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/278,635
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9989
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 479 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-258B-2

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Query Match      2.0%; Score 10; DB 3; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

Qy      236 NLLIPCVLIS 245
      |||||
Db      243 NLLIPCVLIS 252

RESULT 15
US-08-471-961-2
; Sequence 2, Application US/08471961
; Patent No. 6100046
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR

```

```

; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9771
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 479 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-961-2

Query Match 2.0%; Score 10
Best Local Similarity 100.0%; Pred. R 100.0%
Matches 10; Conservative 0; Mismatches 0

QY 236 NLLIPCVLIS 245
|||||
DB 243 NLLIPCVLIS 252
|||||

Search completed: June 20, 2003, 19:15:03
Job time : 29 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2003, 18:52:00 ; Search time 23 Seconds
(without alignments)
905.266 Million cell updates/sec

Title: US-09-954-936-2

Perfect score: 2703

Sequence: 1 MRCSPGVWLALASLLHVS.....TIGILMSAPNFVEAVSKDFA 502

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2698	99.8	502	1	ACH7_HUMAN
2	2545	94.2	502	1	ACH7_MOUSE
3	2536	93.8	499	1	ACH7_BOVIN
4	2531	93.6	502	1	ACH7_RAT
5	2429	89.9	502	1	ACH7_CHICK
6	1107.5	41.0	498	1	ACH1_CAEL
7	960.5	35.5	516	1	ACH1_MANSE
8	947	35.0	557	1	ACH1_SCHGR
9	945	35.0	529	1	ACH2_HUMAN
10	940.5	34.8	511	1	ACH2_RAT
11	938.5	34.7	459	1	ACHN_CARAU
12	937.5	34.7	528	1	ACH2_CHICK
13	935.5	34.6	576	1	ACH2_DROME
14	934	34.6	622	1	ACH4_CHICK
15	932	34.5	503	1	ACH3_HUMAN
16	922	34.1	496	1	ACH3_CHICK
17	922	34.1	567	1	ACH1_DROME
18	916	33.9	627	1	ACH1_HUMAN
19	915.5	33.9	495	1	ACH3_BOVIN
20	913	33.8	495	1	ACHP_RAT
21	908	33.6	630	1	ACH4_RAT
22	901.5	33.4	499	1	ACH3_RAT
23	884	32.7	494	1	ACH6_CHICK
24	884	32.7	498	1	ACHP_HUMAN
25	878	32.5	521	1	ACH3_DROME
26	876.5	32.4	491	1	ACHN_CHICK
27	876	32.4	470	1	ACHP_CHICK
28	874	32.3	512	1	ACH3_CARAU
29	867.5	32.1	450	1	ACHX_HUMAN
30	867.5	32.1	494	1	ACH6_HUMAN
31	862.5	31.9	493	1	ACH6_RAT
32	861	31.9	502	1	ACHN_HUMAN
33	857	31.7	457	1	ACHA_RAT

34	852.5	31.5	479	1	ACH9_HUMAN	O9ugm1 homo sapien
35	850	31.4	457	1	ACHA_MOUSE	P04756 mus musculu
36	849.5	31.4	511	1	ACH5_CAEL	Q23022 caenorhabdi
37	847	31.3	538	1	ACH8_CAEL	P45963 caenorhabdi
38	845	31.3	457	1	ACHA_BOVIN	P02709 bos taurus
39	842	31.2	519	1	ACH4_DROME	P25162 drosophila
40	839	31.0	456	1	ACHA_CHICK	P09479 gallus gall
41	837	31.0	500	1	ACHN_RAT	P12390 rattus norv
42	832.5	30.8	479	1	ACH9_RAT	P43144 rattus norv
43	829.5	30.7	456	1	ACHA_BRARE	Q98880 brachydanio
44	829.5	30.7	457	1	ACH1_XENLA	P22456 xenopus lae
45	822.5	30.4	464	1	ACHO_RAT	P12391 rattus norv

ALIGNMENTS

RESULT 1

ACH7_HUMAN STANDARD; PRT; 502 AA.
AC P36544; Q15826; Q99555; Q96RH2; Q9BXH0;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
GN CHRNA7 OR NACHRA7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RC MEDLINE=94195283; PubMed=8145738;
RA Peng X., Katz M., Gerzanich V., Anand R., Lindstrom J.;
RT "Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit
from the SH-SY5Y cell line and determination of pharmacological
properties of native receptors and functional alpha 7 homomers
expressed in Xenopus oocytes.";
RT Mol. Pharmacol. 45:546-554(1994).
RL [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Hippocampus;
RC Logel J., Drebing C., Barnhart M., Antle C., Leonard S.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97062879; PubMed=8906617;
RA Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
RT Chavez-Noriega L.E., Johnson E.C., Velicellebi G., Harpold M.M.;
RT "Comparative structure of human neuronal alpha 2-alpha 7 and beta
2-beta 4 nicotinic acetylcholine receptor subunits and functional
RT expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
beta 4 subunits.";
RT J. Mol. Neurosci. 7:217-228(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97162233; PubMed=9009220;
RA Groot Kormelink P.J., Luyten W.H.M.L.;
RT "Cloning and sequence of full-length cDNAs encoding the human neuronal
RT nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and
RT expression of seven nAChR subunits in the human neuroblastoma cell
RT line SH-SY5Y and/or IMR-32.";
RT FEBS Lett. 400:309-314(1997).
RN [5]
RP REVISIONS.
RA Groot Kormelink P.J., Luyten W.H.M.L.;
RN Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Epidermal keratinocytes;
RA Arredondo J., Grando S.A.;
RT "Cloning cholinergic receptors in human keratinocytes.";

Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 [7] SEQUENCE OF 17-502 FROM N.A.
 RP TISSUE=Brain;
 RC Doucette-Stamm L., Monteggia L.M., Donnelly-Roberts D., Wang M.T.,
 RA Lee J., Tian J., Giordano T.;
 RT "Cloning and sequence of the human a7 nicotinic acetylcholine
 receptor.";
 RL Drug Dev. Res. 30:252-256(1993).
 [8]
 RP SEQUENCE OF 24-502 FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=94245114; PubMed=8188270;
 RA Chini B., Raimondi E., Elgoyhen A.B., Moralli D., Balzaretto M.,
 RA Heinemann S.F.;
 RT "Molecular cloning and chromosomal localization of the human alpha 7-
 nicotinic receptor subunit gene (CHRNA7).";
 RL Genomics 19:379-381(1994).
 [9]
 RP SEQUENCE OF 118-129 FROM N.A.
 RX PubMed=11829490;
 RA Riley B., Williamson M., Collier D., Wilkie H., Makoff A.;
 RT "A 3-Mb map of a large segmental duplication overlapping the alpha7-
 nicotinic acetylcholine receptor gene (CHRNA7) at human 15q13-q14.";
 RL Genomics 79:197-209(2002).
 [10]
 RP MASS SPECTROMETRY.
 RC TISSUE=Breast cancer;
 RX MEDLINE=21829512; PubMed=11840567;
 RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
 RA Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
 RA Zvelebil M.J.;
 RT "Cluster analysis of an extensive human breast cancer cell line
 protein expression map database.";
 RL Proteomics 2:212-223(2002).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
 CC BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
 CC SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- MASS SPECTROMETRY: MW=54157.68; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC
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 CC
 CC EMBL; X70297; CAA49778.1; -;
 DR EMBL; U40583; AAA83561.1; -;
 DR EMBL; U62436; AAB40114.1; -;
 DR EMBL; Y08420; CAA69697.1; -;
 DR EMBL; AF385585; AAK68111.1; -;
 DR EMBL; L25827; -; NOT ANNOTATED_CDS.
 DR EMBL; Z23141; CAA80672.1; -;
 DR EMBL; AF332758; AAK19515.1; -;
 DR Genew; HGNC:1960; CHRNA7.
 DR MIM; 118511; -;
 DR InterPro; IPR000188; GABAA receptor.
 DR InterPro; IPR001175; Neur Channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_mem; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
 DR Posttranslational modification; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.

FT SIGNAL 1 22 BY SIMILARITY.
 FT CHAIN 23 502 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT ALPHA-7 CHAIN.
 FT DOMAIN 23 230 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 231 255 POTENTIAL.
 FT TRANSMEM 262 280 POTENTIAL.
 FT TRANSMEM 296 317 POTENTIAL.
 FT DOMAIN 318 469 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 470 490 POTENTIAL.
 FT DISULFID 150 164 BY SIMILARITY.
 FT DISULFID 212 213 ASSOCIATED WITH RECEPTOR ACTIVATION
 FT (BY SIMILARITY).
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 11 11 A -> G (IN REF. 1 AND 7).
 FT CONFLICT 58 58 S -> N (IN REF. 2 AND 6).
 FT CONFLICT 134 134 S -> P (IN REF. 2 AND 6).
 FT CONFLICT 364 364 C -> S (IN REF. 8).
 FT CONFLICT 375 375 A -> G (IN REF. 1).
 FT CONFLICT 409 413 RMACS -> AWPAP (IN REF. 8).
 SQ SEQUENCE 502 AA; 56449 MW; D94B3A482EAA0E42 CRC64;
 Query Match 99.8%; Score 2698; DB 1; Length 502;
 Best Local Similarity 99.8%; Pred. No. 2.3e-213;
 Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MRCSPGGVWLALAAASLHVSLQGFQRLKYLKYNYNPLRPVANDSQPLTVYFSL 60
 Db 1 MRCSPGGVWLALAAASLHVSLQGFQRLKYLKYNYNPLRPVANDSQPLTVYFSL 60
 Qy 61 QIMVDVSKNOVLTNNIWLQSWTDHYLQWNVSEYPGVKTVPDQGWKPDILLVNSADE 120
 Db 61 QIMVDVSKNOVLTNNIWLQSWTDHYLQWNVSEYPGVKTVPDQGWKPDILLVNSADE 120
 Qy 121 RFDATEFTNNLVNSSGHGCOYLPPGIFKSSCYIDVRWFPFDVQHCKLFGSGWSYGL 180
 Db 121 RFDATEFTNNLVNSSGHGCOYLPPGIFKSSCYIDVRWFPFDVQHCKLFGSGWSYGL 180
 Qy 181 QMQEADISGYIPNGEWDLVGIPGRSRFYECCKEYPDPVTFVTMRRTLYYGLNLLIP 240
 Db 181 QMQEADISGYIPNGEWDLVGIPGRSRFYECCKEYPDPVTFVTMRRTLYYGLNLLIP 240
 Qy 241 CVLISALALLVFLPADSGEKISIGITVLLSLTFMLLVAEIMPATSDVPLIAQYFAS 300
 Db 241 CVLISALALLVFLPADSGEKISIGITVLLSLTFMLLVAEIMPATSDVPLIAQYFAS 300
 Qy 301 MIIVGLSVVTVIVLQYHHDDPDGCKMPKWRVILLNWCANFLMRKRPGEKVRPACQHK 360
 Db 301 MIIVGLSVVTVIVLQYHHDDPDGCKMPKWRVILLNWCANFLMRKRPGEKVRPACQHK 360
 Qy 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGRMACSPHDBL 420
 Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGRMACSPHDBL 420
 Qy 421 LHGGQPPGDDDLAKILEEYVIANRFRQDESEAVCSEWFAACVVDRLCLMAFVSFTI 480
 Db 421 LHGGQPPGDDDLAKILEEYVIANRFRQDESEAVCSEWFAACVVDRLCLMAFVSFTI 480
 Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
 Db 481 ICTIGILMSAPNFVEAVSKDFA 502
 RESULT 2
 ACH7 MOUSE
 ID ACH7_MOUSE STANDARD; PRT; 502 AA.
 AC P49582;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
 GN CHRNA7 OR ACRA7.

OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=BAUB/C; TISSUE=Brain;	
RX	MEDLINE=95324936; PubMed=7604470;	
RA	Ort-Urtreger A., Seldin M.F., Baldini A., Beaudet A.L.;	
RT	"Cloning and mapping of the mouse alpha 7-neuronal nicotinic	
RT	acetylcholine receptor.";	
RL	Genomics 26:399-402(1995).	
CC	-1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN	
CC	EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND	
CC	LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA	
CC	MEMBRANE.	
CC	-1- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-	
CC	BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY	
CC	SIMILARITY).	
CC	-1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.	
CC	-----	
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CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC	or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL; L37663; AAC42053.1; --	
DR	MGD; MGI:99779; Chnra7.	
DR	InterPro; IPR000188; GABAA receptor.	
DR	InterPro; IPR001175; Neur Channel.	
DR	Pfam; PF02931; Neur_chan_IBD; 1.	
DR	Pfam; PF02932; Neur_chan_membr; 1.	
DR	PRINTS; PR00252; NRIONCHANNEL.	
DR	TIGRFAMS; TIGR00860; LIC; 1.	
DR	PROSITE; PS00236; NEUROTR ION CHANNEL; 1.	
DR	Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;	
KW	Transmembrane; Multigene family.	
FT	SIGNAL 1 22	
FT	CHAIN 23 502	
FT	FT	
FT	DOMAIN 23 230	
FT	TRANSMEM 231 255	
FT	TRANSMEM 262 280	
FT	TRANSMEM 296 317	
FT	DOMAIN 318 469	
FT	TRANSMEM 470 490	
FT	DISULFID 150 164	
FT	DISULFID 212 213	
FT	FT	
FT	CARBOHYD 46 46	
FT	CARBOHYD 90 90	
FT	CARBOHYD 133 133	
FT	SEQUENCE 502 AA; 56631 MW; C9312E5226D120B3 CRC64;	
SEQ		
Query Match 94.2%; Score 2545; DB 1; Length 502;		
Best Local Similarity 93.8%; Pred. No. 7.6e-201;		
Matches 466; Conservative 18; Mismatches 13; Indels 0; Gaps 0;		
QY	6 GGWLALAAALLHVSILQGEFORLYKELVKNYNPLRPVANDSOPLTVYFSLSLQIMDV 65	
DB	6 GGWLALAAALLHVSILQGEFORLYKELVKNYNPLRPVANDSOPLTVYFSLSLQIMDV 65	
QY	66 DEKNQVLTNNILQMSWTHYLQWNSYSEYGVKTVRFPDQGIWKPDILLYNSADERFAT 125	
DB	66 DEKNQVLTNNILQMSWTHYLQWNSYSEYGVKTVRFPDQGIWKPDILLYNSADERFAT 125	
QY	126 FHTNVLVNSGHCQYLPDGIKFSKSSCIDVRWPFVDVQVCKLKFGSGSYGWSLDLQMOEA 185	
DB	126 FHTNVLVNSGHCQYLPDGIKFSKSSCIDVRWPFVDVQVCKLKFGSGSYGWSLDLQMOEA 185	

OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=BAUB/C; TISSUE=Brain;	
RX	MEDLINE=95324936; PubMed=7604470;	
RA	Ort-Urtreger A., Seldin M.F., Baldini A., Beaudet A.L.;	
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RT	acetylcholine receptor.";	
RL	Genomics 26:399-402(1995).	
CC	-1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN	
CC	EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND	
CC	LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA	
CC	MEMBRANE.	
CC	-1- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-	
CC	BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY	
CC	SIMILARITY).	
CC	-1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.	
CC	-----	
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC	or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL; L37663; AAC42053.1; -	
DR	MGD; MGI:99779; Chnra7.	
DR	InterPro; IPR000188; GABAA receptor.	
DR	InterPro; IPR001175; Neur Channel.	
DR	Pfam; PF02931; Neur_chan_LBD; 1.	
DR	Pfam; PF02932; Neur_chan_membr; 1.	
DR	PRINTS; PR00252; NRIONCHANNEL.	
DR	TIGRFAMS; TIGR00860; LIC; 1.	
DR	PROSITE; PS00236; NEUROTR ION CHANNEL; 1.	
DR	Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;	
KW	Transmembrane; Multigene family.	
FT	SIGNAL 1 22	
FT	CHAIN 23 502	
FT	FT	
FT	DOMAIN 23 230	
FT	TRANSMEM 231 255	
FT	TRANSMEM 262 280	
FT	TRANSMEM 296 317	
FT	DOMAIN 318 469	
FT	TRANSMEM 470 490	
FT	DISULFID 150 164	
FT	DISULFID 212 213	
FT	FT	
FT	CARBOHYD 46 46	
FT	CARBOHYD 90 90	
FT	CARBOHYD 133 133	
FT	SEQUENCE 502 AA; 56631 MW; C9312E5226D120B3 CRC64;	
SEQ		
Query Match	94.2%; Score 2545; DB 1; Length 502;	
Best Local Similarity	93.8%; Pred. No. 7.6e-201;	
Matches 466; Conservative 18; Mismatches 13; Indels 0; Gaps 0;		
QY	6 GGWLALAAALLHVSILQGEFORLYKELVKNYNPLRPVANDSOPLTVYFSLSLQIMDV 65	
DB	6 GGWLALAAALLHVSILQGEFORLYKELVKNYNPLRPVANDSOPLTVYFSLSLQIMDV 65	
QY	66 DEKNQVLTNNIQLQMSWTHYLQWNSYSEYGVKTVRFPDQGIWKPDILLYNSADERFDAT 125	
DB	66 DEKNQVLTNNIQLQMSWTHYLQWNSYSEYGVKTVRFPDQGIWKPDILLYNSADERFDAT 125	
QY	126 FHTNVLVNSGHCQYLPDGIKFSKSSCIDVRWPFVDVQHCKLKFGSGSYGWSLDLQMOEA 185	
DB	126 FHTNVLVNSGHCQYLPDGIKFSKSSCIDVRWPFVDVQHCKLKFGSGSYGWSLDLQMOEA 185	

DR EMBL; X93604; CAAC3802.1; --
DR InterPro; IPR000188; GABAA receptor.
DR InterPro; IPR001175; Neur Channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
DR Post-synaptic membrane; Ionic Channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family; Alternative splicing.
FT SIGNAL 1 19
FT CHAIN 20 499
FT
FT DOMAIN 20 227
FT TRANSMEM 28 252
FT TRANSMEM 259 277
FT TRANSMEM 293 314
FT DOMAIN 315 466
FT TRANSMEM 467 487
FT DISULFID 147 161
FT DISULFID 209 210
FT
FT CARBOHYD 43 43
FT CARBOHYD 87 87
FT CARBOHYD 130 130
FT VARSPLIC 262 290
SQ SEQUENCE 499 AA; 56002 MW; ABE5D0B3820D42D5 CRC64;
Query Match 93.8%; Score 2536; DB 1; Length 499;
Best Local Similarity 94.4%; Pred. No. 4.1e-200;
Matches 469; Conservative 15; Mismatches 13; Indels 0; Gaps 0;
QY 6 GGWTLAASLLHVSLOGEQRKLYKLVNKNYPLRPVANDSOPLYFSLSLQIMDV 65
Db 3 GSICLAASILHVSLOGEQRKLYKLVNKNYPLRPVANDSOPLYFSLSLQIMDV 62
QY 66 DEKNQVLTNIWLQMSWTDRYLOWNYSYPGVKTVRPDGIQWPKDILLNSADERFDT 125
Db 63 DEKNQVLTNIWLQMTWDRYLOWNYSYPGVKTVRPDGIQWPKDILLNSADERFDT 122
QY 126 FHTNVLNNSGHCQYLPPIGIFKSSCYIDVRWFPDQVQCKLKFGSWSYGWSLQMQEA 185
Db 123 FHTNVLNNSGHCQYLPPIGIFKSSCYIDVRWFPDQVQCKLKFGSWSYGWSLQMQEA 182
QY 186 DISGYIPNGEWDLVGIPKGSERFYECKEPPYDVTFTVWRRRTLYGLNLLIPCVLLIS 245
Db 183 DISGYIPNGEWDLVGVLGKSEKFEYCKEPPYDVTFTVWRRRTLYGLNLLIPCVLLIS 242
QY 246 ALALLVFLPADSGEKISLGLTVLLSLTTTMLVAETMPATSDSVPLIAQYFASMTIIVG 305
Db 243 ALALLVFLPADSGEKISLGLTVLLSLTVFLLVAETMPATSDSVPLIAQYFASMTIIVG 302
QY 306 LSVVTVTVILQYHHDDPGGKMPKWTRVIIILNWCWFLRMKRPGEKVRPACQHKQRCS 365
Db 303 LSVVTVTVILQYHHDDPGGKMPKWTRVIIILNWCWFLRMKRPGEKVRPACQHKQRCS 362
QY 366 LASVMSAVAPPASNNLYIGRGLDGVHCVTPDPSGVVCGVMACSPTHDEHLLHGQ 425
Db 363 LASVMSAVAGPATNGNLLYIGRGLDGVHCVTPDPSGVVCGVMACSPTHDEHLLHAGQ 422
QY 426 PPSGDDPLAKLIEVRVYIANFRFCODESEAVCEWKEAACVVDRLCLMAFVFTLCTIG 485
Db 423 PPSGDDPLAKLIEVRVYIANFRFCODESEAVCEWKEAACVVDRLCLMAFVFTLCTIG 482
QY 486 ILSAPNFVEAVSKDFA 502
Db 483 ILSAPNFVEAVSKDFA 499
RESULT 4
ACH7 RAT
ID ACH7 RAT
AC Q05941;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
GN CHRNA7 OR ACRA7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RC MEDLINE=931147931; PubMed=7678857;
RA Seguela P., Wadiche J., Dineley-Miller K., Dani J.A., Patrick J.W.;
RT "Molecular cloning, functional properties, and distribution of rat
brain alpha 7: a nicotinic cation channel highly permeable to
calcium.";
RL J. Neurosci. 13:596-604(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley; TISSUE=Brain;
RA Boulter J.;
RT Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RC REVISION TO 363.
RA STRAIN=Sprague-Dawley; TISSUE=Brain;
RL Hartley M.;
RT Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
CC BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; S53987; AAR25224.2; --
CC EMBL; L31619; AAC33136.1; --
DR InterPro; IPR000188; GABAA receptor.
DR InterPro; IPR001175; Neur Channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
DR Post-synaptic membrane; Ionic Channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 22
FT CHAIN 23 502
FT
FT DOMAIN 23 230
FT TRANSMEM 231 255
FT TRANSMEM 262 280
FT TRANSMEM 296 317
FT DOMAIN 318 469
FT TRANSMEM 470 490
FT DISULFID 150 164
FT DISULFID 212 213
FT
FT CARBOHYD 46 46
FT CARBOHYD 90 90
FT CARBOHYD 133 133
FT CONFLICT 447 447
N -> F (IN REF. 2).

FT CONFLICT 469 469 P -> R (IN REF. 2).
 SQ SEQUENCE 502 AA; 56410 MW; 00996574EC7B9A56 CRC64;
 Query Match 93.6%; Score 2531; DB 1; Length 502;
 Best Local Similarity 93.4%; Pred. No. 1.1e-199;
 Matches 464; Conservative 18; Mismatches 15; Indels 0; Gaps 0;
 QY 6 GGWLALAAALLHVSLOGEQRKLYKELVKNYNPLERPVANDSOPLTVYFSLSLQIMDV 65
 DB 6 GGWLALAAALLHVSLOGEQRKLYKELVKNYNPLERPVANDSOPLTVYFSLSLQIMDV 65
 QY 66 DEKNQVLTNIWLQMSWTDHYLQWNVSEYPGVKTVRPDGOIWKPDILLVNSADERFDAT 125
 DB 66 DEKNQVLTNIWLQMSWTDHYLQWNVSEYPGVKTVRPDGOIWKPDILLVNSADERFDAT 125
 QY 126 FHTNVLVNSGHCHQYLPPIGFKSSCYIDVRWFPDVOHQCKLKFGSWSYGSLSLQMOEA 185
 DB 126 FHTNVLVNSGHCHQYLPPIGFKSSCYIDVRWFPDVOHQCKLKFGSWSYGSLSLQMOEA 185
 QY 186 DISGYIPNGEWDLVGIPGKSERFYECKEPPYDVTFTVWRRRTLYGLNLLIPCVLLIS 245
 DB 186 DISGYIPNGEWDLVGIPGKSERFYECKEPPYDVTFTVWRRRTLYGLNLLIPCVLLIS 245
 QY 246 ALALLVFLPADSGEKISLIGITVLLSTTMTMLVAEIMPATSDSPVLIQAQYFASTMIIVG 305
 DB 246 ALALLVFLPADSGEKISLIGITVLLSTTMTMLVAEIMPATSDSPVLIQAQYFASTMIIVG 305
 QY 306 LSVVVTVIVLQYHHHPDGGKMPKWTIVILNWCWFLRMKPGEDKVRPACQKQRRC 365
 DB 306 LSVVVTVIVLQYHHHPDGGKMPKWTIVILNWCWFLRMKPGEDKVRPACQKQRRC 365
 QY 366 LASVENSAPPASNGNLLYIGFRGLDGVHCVTPDPSGVVCGRMACSPTHDEHLRHGG 425
 DB 366 LASVELSAGAPPTSGNLLYIGFRGLEGMHCAPTDPDSGVVCGRLACSPTHDEHLMHGAH 425
 QY 426 PEGDPLAKILEVRYIANRFRQDESEAVCSWKFAACVVDRLCLMAVSFTIITIG 485
 DB 426 PSDGDPDLAKILEVRYIANRNRQDESEVICSEWKEFAACVVDPLCLMAVSFTIITIG 485
 QY 486 ILMSAPNFVEAVSKDFA 502
 DB 486 ILMSAPNFVEAVSKDFA 502

RESULT 5

ACH7 CHICK STANDARD; PRT; 502 AA.
 ID ACH7 CHICK STANDARD; PRT; 502 AA.
 AC P22770;
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=91097796; PubMed=1702646;
 RA Couturier S., Bertrand D., Matter J.M., Hernandez M.C., Bertrand S.,
 RA Millar N., Valera S., Barkas T., Ballivet M.;
 RT "A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is
 RT developmentally regulated and forms a homo-oligomeric channel blocked
 RT by alpha-BTX.";
 RL Neuron 5:847-856(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=90315158; PubMed=2369519;
 RA Schoepfer R., Conroy W.G., Whiting P., Gore M., Lindstroem J.;
 RT "Brain alpha-bungarotoxin binding protein cDNAs and MADS reveal

RT subtypes of this branch of the ligand-gated ion channel gene
 RL superfamily.";
 RN Neuron 5:35-48(1990).
 RN [3]
 RP SEQUENCE OF 1-18 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93049204; PubMed=1425587;
 RA Matter-Sadzinski L., Hernandez M.C., Rostocil T., Ballivet M.,
 RA Matter J.M.;
 RT "Neuronal specificity of the alpha 7 nicotinic acetylcholine receptor
 RT promoter develops during morphogenesis of the central nervous
 RL system.";
 RN EMBO J. 11:4529-4538(1992).
 RN [4]
 RP SEQUENCE OF 24-47.
 RC TISSUE=Brain;
 RX MEDLINE=85270494; PubMed=3860855;
 RA Conti-Tronconi B.M., Dunn S.M.J., Barnard E.A., Dolly J.O., Lai F.A.,
 RA Ray N., Raftery M.A.;
 RT "Brain and muscle nicotinic acetylcholine receptors are different but
 RT homologous proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:5208-5212(1985).
 RN [5]
 RP MUTAGENESIS OF LEU-270.
 RX MEDLINE=92049732; PubMed=1719423;
 RA Recah F., Bertrand D., Galzi J.-L., Devillers-Thiery A., Mulle C.,
 RA Hussy N., Bertrand S., Ballivet M., Changeux J.-P.;
 RT "Mutations in the channel domain alter desensitization of a neuronal
 RT nicotinic receptor.";
 RL Nature 353:846-849(1991).
 RN [6]
 RP MUTAGENESIS TO CONVERT ION SELECTIVITY FROM CATIONIC TO ANIONIC.
 RX MEDLINE=93024917; PubMed=1383829;
 RA Galzi J.-L., Devillers-Thiery A., Hussy N., Bertrand S.,
 RA Changeux J.-P., Bertrand D.;
 RT "Mutations in the channel domain of a neuronal nicotinic receptor
 RT convert ion selectivity from cationic to anionic.";
 RL Nature 359:500-505(1992).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
 CC BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
 CC SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- DEVELOPMENTAL STAGE: ALPHA-7 TRANSCRIPTS TRANSIENTLY ACCUMULATE
 CC IN THE DEVELOPING OPTIC TECTUM BETWEEN E5 AND E16.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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 CC -----
 CC EMBL; X52295; CAA36543.1; -;
 CC EMBL; X68246; CAA48317.1; -;
 CC EMBL; X68586; CAA48576.1; -;
 CC PIR; JN0113; JN0113.
 CC PIR; B25738; B25738.
 CC PIR; JH0172; JH0172.
 CC InterPro; IPR000188; GABA_A receptor.
 CC InterPro; IPR001175; Neur channel.
 CC PIR; PF02931; Neur_chan_IID; 1.
 CC PIR; PF02932; Neur_chan_IID; 1.
 CC PRINTS; PR00252; NRIONCHANNEL.
 CC TIGRFAMs; TIGR00860; LIC; 1.
 CC PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
 CC Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 CC Transmembrane; Multigene family.
 KW


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FT SIGNAL 1 23
FT CHAIN 24 502
FT FT NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
FT FT ALPHA-7 CHAIN.
FT FT EXTRACELLULAR.
FT DOMAIN 24 230
FT TRANSMEM 231 255
FT TRANSMEM 262 280
FT TRANSMEM 296 317
FT DOMAIN 318 469
FT TRANSMEM 470 490
FT DISULFID 150 164
FT DISULFID 212 213
FT FT
FT CARBOHYD 46 46
FT CARBOHYD 90 90
FT CARBOHYD 133 133
FT MUTAGEN 270 270
FT FT
FT CONFLICT 26 27
FT SEQUENCE 502 AA; 56946 MW; 572325D4309AD2FD CRC64;
SQ
Query Match 89.9%; Score 2429; DB 1; Length 502;
Best Local Similarity 90.7%; Pred. No. 2.4e-191;
Matches 449; Conservative 19; Mismatches 28; Indels 0; Gaps 0;
QY 8 VWLALASLHVSLQGEFQRLKYLKYNPNLPRVANDSQPLTVYFSLSLQIMDVDE 67
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
8 LWLALAAGLVRESLQGEFQRLKYLKYNPNLPRVANDSQPLTVYFSLSLQIMDVDE 67
QY 68 KNOVLTTNIWQSWTDHYLQWNVSEYPGVKTVPDGOIWKPDILLYNSADERFDATFH 127
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
68 KNOVLTTNIWQSWTDHYLQWNVSEYPGVKTVPDGOIWKPDILLYNSADERFDATFH 127
QY 128 TNLVNSSGHCOYLPFGIFKSSCYIDVRWPFEDVOHCKLFGSGWSYGLDLOMOEADI 187
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
128 TNLVNSSGHCOYLPFGIFKSSCYIDVRWPFEDVOHCKLFGSGWSYGLDLOMOEADI 187
QY 188 SGYIPNGEWDLVGPGRKSRFECCKEYPDVTFTVTMRRRTLYYGLNLLIPCVLISAL 247
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
188 SGYIPNGEWDLVGPGRKSRFECCKEYPDVTFTVTMRRRTLYYGLNLLIPCVLISAL 247
QY 248 ALLVFLPADSGEKISIGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFASMTIIVGLS 307
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
248 ALLVFLPADSGEKISIGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFASMTIIVGLS 307
QY 308 VVTVTVLVQYHHDDPGCKPKTRVILLNWKAFLEMKRPGEDKVPACQHKORCSLA 367
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
308 VVTVTVLVQYHHDDPGCKPKTRVILLNWKAFLEMKRPGEDKVPACQHKORCSLS 367
QY 368 SVMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDGCVGGRMACSPTHDEHLLHGGOPP 427
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
368 SVMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDGCVGGRMACSPTHDEHLLHGGOPP 427
QY 428 EGPDPDLAKILEEVRYIANRFRQDESEAVCSWKFAACVVDRLCLMAFVSFTIICIGIL 487
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
428 EGPDPDLAKILEEVRYIANRFRQDESEAVCSWKFAACVVDRLCLMAFVSFTIICIGIL 487
QY 488 MSAPNFVEAVSKDFA 502
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
488 MSAPNFVEAVSKDFA 502

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RESULT 6

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ID ACHI_CABEL STANDARD; PRT; 498 AA.
AC P48180;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acetylcholine receptor like protein, alpha-type chain precursor.
GN F25G6.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.

```

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OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=96196478; PubMed=8627624;
RA Ballivet M., Alliod C., Bertrand S., Bertrand D.;
RT "Nicotinic acetylcholine receptors in the nematode Caenorhabditis elegans.";
RL J. Mol. Biol. 258:261-269 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Nelson J., Wohldmann P.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: POSSIBLE ACETYLCHOLINE RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC
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CC
CC EMBL; X83887; CAA58764.1; -.
DR EMBL; AF022973; AAC25796.1; -.
DR HSP; P58154; 119B.
DR WormPep; F25G6.3; CE09639.
DR InterPro; IPR001188; GABAA receptor.
DR InterPro; IPR001175; Neur. Channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_mem; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
DR Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane; signal.
FT SIGNAL 19
FT CHAIN 20 498
FT FT POTENTIAL.
FT FT ACETYLCHOLINE RECEPTOR LIKE PROTEIN,
FT FT ALPHA-TYPE CHAIN.
FT FT EXTRACELLULAR (POTENTIAL).
FT FT
FT FT POTENTIAL.
FT FT TRANSMEM 231 252
FT FT TRANSMEM 261 279
FT FT TRANSMEM 295 314
FT FT DOMAIN 315 472
FT FT TRANSMEM 473 493
FT FT DISULFID 147 161
FT FT DISULFID 211 212
FT FT
FT FT CARBOHYD 43 43
FT FT CARBOHYD 93 93
FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 498 AA; 57169 MW; E463ABB40AC9FA82 CRC64;
Query Match 41.0%; Score 1107.5; DB 1; Length 498;
Best Local Similarity 44.6%; Pred. No. 3.8e-83;
Matches 226; Conservative 77; Mismatches 167; Indels 37; Gaps 7;
QY 10 LALAASLHVSLQGEFQ-RKLYKELVKNYNLPRVANDSQPLTVYFSLSLQIMDVDEK 68
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
6 LLISCAILAAPTLSLQERRLYEDLMRNYNLPRVANDSQPLTVYFSLSLQIMDVDEK 65
QY 69 NOVLTTNIWQSWTDHYLQWNVSEYPGVKTVPDGOIWKPDILLYNSADERFDATFH 128
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
66 NOVVVNAWLDYTWNDYLVNDKAEYGNITDVRFPAGKIWKPDILLYNSVDTNFDSTYTQ 125
QY 129 NVLVNSSGHCOYLPFGIFKSSCYIDVRWPFEDVOHCKLFGSGWSYGLDLOMOEADI 186
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
126 NMIVYSTGLVHWVPPGIFKISKIDIQWFPDEQCKFFKGSWTYDGYKLDLPATGGFD 185
QY 187 ISGYIPNGEWDLVGPGRKSRFECCKEYPDVTFTVTMRRRTLYYGLNLLIPCVLISA 246
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 186 ISEYISNGEWALPLTTVERNEKFYDCCPEYDPVHFLHMRRTLYYGFNLMPICILFTL 245
 QY 247 LALLVLLPADSGEKISLIGITVLLSLTFTMLLVAEIMPATSDSVPLIAQYFASFTMIIVGL 306
 Db 246 MTLGLGFLPADAGEKITLQITVLLSICFFLSIVSEMSPTSEAVPLLGIFFTCCMIVVTA 305
 QY 307 SVVTVTVLVQVHHDPDGGKMKWTRVILLNWCWFLRMKRPDGVKVRPACQKQRCSL 366
 Db 306 STVFTVTVLVNLTPTHTDMPWTRNLLLVWIPWILRMKRPD-----HMLTVASL 356
 QY 367 ASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDS-----GVVCGRMAC 412
 Db 357 PSL-----FSTKPNRHSLSLRNIK--DNEHSLSRANSFADACRLNQYIMTQSVSNGLTSL 410
 QY 413 SPTHDEHLHGQPPGEGDPD-----LAKILEEVIYANRFRQDESEAVCSEWKPACVW 467
 Db 411 GSIPSTMISSNGTTTVDVSOQATLLHLRIYHELKIYVTRMIEGDKKEQACNNKWFAMV 470
 QY 468 DRCLMAFVSFTIICITIGILMSAFNV 494
 Db 471 DRCLVFTTIIIVSTIGIFWSPALV 497

RESULT 7

ACH1 MANSE
 ID ACH1 MANSE STANDARD; PRT; 516 AA.
 AC P91766;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acetylcholine receptor protein, alpha-like chain precursor (MARAL).
 GN ARAL.
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
 OC Ditrysia; Sphingioidea; Sphingidae; Sphinginae; Manduca.
 OX NCBI_TaxID=7130;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98424077; PubMed=9753155;
 RA Eastham H.M., Lind R.J., Eastlake J.L., Clarke B.S., Towner P.,
 RA Reynolds S.E., Wolstenholme A.J., Wonnacott S.;
 RT "Characterization of a nicotinic acetylcholine receptor from the
 insect Manduca sexta";
 RL Eur. J. Neurosci. 10:879-889(1998).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC -----
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 CC -----
 CC EMBL; Y09795; CAA70928.1; -
 DR InterPro; IPR000188; GABAA Receptor.
 DR InterPro; IPR001175; Neur Channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PRO0252; NRIONCHANNEL.
 DR TIGRFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
 KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 516 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-
 FT LIKE CHAIN.

FT DOMAIN 22 243 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 244 264 POTENTIAL.
 FT TRANSMEM 274 294 POTENTIAL.
 FT TRANSMEM 306 326 POTENTIAL.
 FT DOMAIN 327 465 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 466 486 POTENTIAL.
 FT DISULFID 149 163 BY SIMILARITY.
 FT DISULFID 222 223 ASSOCIATED WITH RECEPTOR ACTIVATION
 (BY SIMILARITY).
 FT CARBOHYD 45 45 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 233 233 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 516 AA; 58720 MW; E7A71B8C45D13BD2 CRC64;
 Query Match 35.5%; Score 960.5; DB 1; Length 516;
 Best Local Similarity 40.4%; Pred. No. 4.3e-71;
 Matches 196; Conservative 88; Mismatches 166; Indels 35; Gaps 6;
 QY 27 RLYKELVKNYPLRPVANDSOPLTVYFSLQLQIMVDKQVLTNINWLOMSWTDHY 86
 Db 26 KRLYDDLLSNYKLVRPVLYNSDALTVRIKLSQLIDVNLKNQIMTNLWTEQSWDYK 85
 QY 87 LQNVSEYVPGVKTFRFPDQIWKPDILLYNSADERFDATEHTNVLVNSSGHCQYLPPIG 146
 Db 86 LSWEPREYGGVEMLHVPSDHIWRPDIYLNADGNFVTLATKATNTYGRVEMRPPIY 145
 QY 147 KSSCYIDVRWFFPDVQCKLXFGSNGSLDQMQE-----ADISGYIPNGE 195
 Db 146 KSSCEIDVEYFPDQTCVMKFGSWTYDGFQDLRHRIDEVRGTNNVELGVDSLSEYTSVE 205
 QY 196 WDLVGIPOKRSEFYECCKEYPDVTFTVWRRRTLYGLNLLIPCVLISALALLVFLP 255
 Db 206 WDILEVPAVRNEKFYTCDEPYLDITFNITRRKTLFTVNLIIIPCMGISFLTVLVFLP 265
 QY 256 ADSGKSLGTLVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASFTMIIVGLSVVTVVL 315
 Db 266 SDGKSVLSISILLSTLVFFLLABIIPTLSLVVPLLGKFLVFTMLDTSICVTVVVL 325
 QY 316 QYHHHDPDGGKVPKWRVILLNWCWFLRMKRPDGVKVRPACQKQRCSLASVMSAVA 375
 Db 326 NVHFRSQTHMSFWRVFTHVLPRLVMRP-HYRLDP---HRSRAGLV- 374
 QY 376 PPPASNGNLLYIGFRGLDGVHCVTPDGSVVVCGR-----MACSPTHDEHLHGQPPGD 430
 Db 375 --GAGETTLWDEGSPG-----VPAPRPPPCAPLAPCAACAPAEAPALCALRRWHRC 426
 QY 431 PDLAKILEEVIYANRFRQDESEAVCSEWKPACVDRCLMAFVSFTIICITIGILMSA 490
 Db 427 PELHKAIDGINYIADQTRKEEESTRVKEDWKYVAMVLDLPFLWIFTLAVVVGSAIILQA 486
 QY 491 PNFVE 495
 Db 487 PTLVD 491

RESULT 8

ACH1 SCHGR
 ID ACH1 SCHGR STANDARD; PRT; 557 AA.
 AC P23414;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acetylcholine receptor protein, alpha-L1 chain precursor.
 OS Schistocerca gregaria (Desert locust).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
 OC Acridomorpha; Acridoidea; Acrididae; Cyrtacanthacridinae;
 OC Schistocerca
 OX NCBI_TaxID=7010;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91092263; PubMed=1702381;
 RA Marshall J., Buckingham S.D., Lunt G.G., Goosey M.W.,

RA Darlison M.G., Sattelle D.B., Barnard E.A.;
RT "Sequence and functional expression of a single alpha subunit of an
RL insect nicotinic acetylcholine receptor.";
EMBO J. 9:4391-4398(1990).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC
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CC
CC EMBL; X55439; CAA39081.1; -;
CC PIR; S12359; S12359.
CC InterPro; IPR000188; GABAA_receptor.
CC InterPro; IPR001175; Neur_chan_1.
CC Pfam; PF02931; Neur_chan_LBD; 1.
CC Pfam; PF02932; Neur_chan_memb; 1.
CC PRINTS; PR00252; NRIONCHANNEL.
CC TIGR; TIGR00860; LIC; 1.
CC PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
CC Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 557 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-L1
FT FT CHAIN.
FT FT EXTRACELLULAR.
FT DOMAIN 24 244
FT TRANSMEM 245 266
FT TRANSMEM 274 294
FT TRANSMEM 308 329
FT DOMAIN 330 500
FT TRANSMEM 501 523
FT DISULFID 151 165
FT DISULFID 224 225
FT CARBOHYD 47 47
FT CARBOHYD 235 235 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DOMAIN 382 400 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DOMAIN 406 422 ALA/SER-RICH.
FT DOMAIN 557 557 HIS-RICH.
SQ SEQUENCE 557 AA; 63026 MW; 168389C887DFDF3E CRC64;

Query Match 35.0%; Score 947; DB 1; Length 557;
Best Local Similarity 37.1%; Pred. No. 6.1e-70;
Matches 201; Conservative 92; Mismatches 177; Indels 72; Gaps 6;

QY 5 PGCVLALASLLHVSILQGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMD 64
DB 6 PPMALLLLLLHHHPAAANPAKLYDILLSNYNRLRPVSNNTDVLVKGRLSLQID 65

QY 65 VDERKQVLTNIMQLQSWTHYLOWNVSEPGVTVTRPPDQCIWKPDLILLNSADDERPDA 124
DB 66 LNLKQDQILTNNVLEHEWQDHKFDWPAEYGVTVLYVPSEHIMLPDVLVLYNNADGEYV 125

QY 125 TETHNVLVNSGHCQYLPPIGFKSSCYIDVRWFPDQVQCKLFGSWSYGCWSLDLQ--- 181
DB 126 TWTAKVLLHTGKVVWTPPAIFKSCSDIVRYFFPDQOTCFMKFGSWTYDGDQIDLKHIN 185

QY 182 -----MOEADISGYPNGEWDLVIGPKRSERFVCECKEYPDVTVFTVMRRRTLYY 233
DB 186 QKYDDNKVKVIGIDLREYVPSVENDILGVPAERHEKYPCCAEYPPDIFFNITLRKTLFY 245

QY 234 GLNLLIPCVLSIALALVFLPADSGKISIGITVLLSLTFTFMLLVAEIMPATSDSVPLI 293
DB 246 TVNLIVPCVGSYLSLVFLVPADSGEKALICISILLSTQTMFFLLISIPSTSLALPLL 305

QY 294 AQYFASTMIIVGLSVVTVIVLYQHHHDPDGGKMPKWTFRVILLNWCAMFLMKRPG--- 350

RESULT 9
ACH2_HUMAN
ID ACH2_HUMAN STANDARD; PRT; 529 AA.
AC Q15822; O9HAQ3;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
GN CHRNA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Hypothalamus;
RX MEDLINE=97062879; PubMed=8906617;
RA Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
RA Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
RT "Comparative structure of human neuronal alpha 2-alpha 7 and beta
RT 2-beta 4 nicotinic acetylcholine receptor subunits and functional
RT expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
RT beta 4 subunits.";
RL J. Mol. Neurosci. 7:217-228(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Groot Kormelink P.J.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Blechschmidt K., Rosenthal A.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES
CC OF SUBUNITS: ALPHA AND NON-ALPHA (BETA). ALPHA-2 SUBUNIT CAN BE
CC COMBINED TO BETA-2 OR BETA-4 TO GIVE RISE TO FUNCTIONAL RECEPTORS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC
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CC
CC EMBL; U62431; AAB40109.1; -;
CC EMBL; Y16281; CAA76154.1; -;
CC EMBL; AF311103; -; NOT_ANNOTATED_CDS.

P12389; O08952;
01-OCT-1989 (Rel. 12, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
CHRNA2 OR ACR2.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley; TISSUE=Brain;
MEDLINE=88178113; PubMed=2832952;
Wada K., Ballivet M., Boulter J., Connolly J.G., Wada E.,
Deneris E.S., Swanson L.W., Heinemann S.F., Patrick J.;
"Functional expression of a new pharmacological subtype of brain
nicotinic acetylcholine receptor.";
Science 240:330-334(1988).
[2]
REVIEWS.
STRAIN=Sprague-Dawley; TISSUE=Brain;
Boulter J.;
Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
-I- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
MEMBRANE.
-I- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

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EMBL; LI0077; AABG0900.1; --
EMBL; M20297; AAA40664.1; --
EMBL; M20292; AAA40664.1; JOINED.
EMBL; M20293; AAA40664.1; JOINED.
EMBL; M20294; AAA40664.1; JOINED.
EMBL; M20295; AAA40664.1; JOINED.
EMBL; M20296; AAA40664.1; JOINED.
InterPro; IPR000188; GABA_A receptor.
DR InterPro; IPR001175; Neur channel.
DR Pfam; PF02931; Neur_chan_IbD; 1.
DR Pfam; PF02932; Neur_chan memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUOTR_ION_CHANNEL; 1.
KW Postsynaptic membrane; Ionic Channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 511 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
FT ALPHA-2 CHAIN.
FT DOMAIN 28 241 EXTRACELLULAR.
FT TRANSMEM 242 266 POTENTIAL.
FT TRANSMEM 274 292 POTENTIAL.
FT TRANSMEM 308 329 POTENTIAL.
FT DOMAIN 330 484 CYTOPLASMIC.
FT TRANSMEM 485 503 POTENTIAL.
FT DOMAIN 391 402 POLY-GLU.
FT DISULFID 160 174 BY SIMILARITY.
FT DISULFID 224 225 ASSOCIATED WITH RECEPTOR ACTIVATION
FT (BY SIMILARITY).
FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 212 212 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CONFLICT 494 494 C -> S (IN REF. 1; AAA40664).
SQ SEQUENCE 511 AA; 58611 MW; 3824E83BB01D613B CRC64;

Query Match 34.8%; Score 940.5; DB 1; Length 511;
Best Local Similarity 39.0%; Pred. No. 1.9e-69;
Matches 201; Conservative 82; Mismatches 180; Indels 53; Gaps 9;

QY 8 VN--LALASLLHVSLSQGFQRLKYLKVNPLRPVANDSOPLTAVYFSLSLQIMDV 65
DB 16 LNCILLVPAVLTCQGSHTAEDELFLKFLFGYNRWAPVNTSDVIVRGLSLAQLIDV 75

QY 66 DEKNQVLTNNLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADDERDAT 125
DB 76 DEKNQVMTNNVWLKQWMDYKLRWDPAEFGNVTSLRVPSEMIWIPDIVLYNNADGRAVT 135

QY 126 FHTNVLVNSGHCQYLPPIGIFKSSCIDVRWFFDVQHCCLKFGWSYGGWSLDLQOE- 184
DB 136 HMTKAHLFTGTGVHWYPPAIFYKSSCSIDVTFFPFDQCNCKFKGWSYDKAKIDLEQMER 195

QY 185 -ADISGYIPNGEMLVGIPIGKRSEFVECKEYPDVTFVTWRRRTLYYGLNLLIPCVL 243
DB 196 TVDLKDYWESGEWAIINATGYNSKKYDCCAEYDPDVTYFVIRRLPLFTINLIIPCLL 255

QY 244 ISALALLVFLPADSGEKISLIGITVLISLFTFMVAEIMPATSDSVPLIAQVFASTMI 303
DB 256 ISCLTVLVYFLPSECKEIKTLCISVLLSLTVFULLITEIIPSTSLVPLICEYLLFTMIF 315

QY 304 VGLSVVTVVILQYHHHDPDGKMPKWRVILLNWCAMFLRMKRP-----GDKVRPA 356
DB 316 VTLSIVITVFLNVHRSSTHNNPNWVRVALLGRVPRWLMNRPPLPMELHSGPDLKLS 375

QY 357 COHKQRCSLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPPTDS--GVVCGRMACSP 414
DB 376 PSYHLETNMDAGERBETEBEEDENICV-----CAGLPDSMGLVYG----- 420

QY 415 THDEHLHGG-----OPPEG-----DPDLAKILEEVRYIANFRQDESEAVCS 458
DB 421 -----HGLHLRAMEPEKTPSQASEILLSQIQALKEGVHYADRLSEADASSVKE 473

QY 459 EWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
DB 474 DNKYAMVVDRIELWFLIIVCFGLTGIGLFL--PPFL 507

RESULT 11
ACHN_CARAU STANDARD; PRT; 459 AA.
AC P19370;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, beta-2 chain (GF-beta-2) (Fragment).
DE Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=90384858; PubMed=2402468;
RA Hieber V.C., Bouchey J.E., Agranoff B.W., Goldman D.;
RT "Nucleotide and deduced amino acid sequence of the goldfish neural
RT nicotinic acetylcholine receptor beta-2 subunit.";
RL Nucleic Acids Res. 18:5307-5307(1990).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT
CC TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).

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CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC -----
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CC -----
CC EMBL; X54052; CAA37986.1; -.
DR PIR; S14703; S14703.
DR InterPro; IPR000188; GABAA receptor.
DR InterPro; IPR011175; Neur Channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_mem; 1.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
KW Transmembrane; Multigene family.
FT NON_TER 1 1
FT DOMAIN <1 203 EXTRACELLULAR.
FT TRANSMEM 204 228
FT TRANSMEM 236 254
FT TRANSMEM 270 291
FT DOMAIN 292 421
FT TRANSMEM 422 440
FT CARBOHYD 21 21 N-LINKED (GLCNAC... ) (POTENTIAL).
FT DISULFID 125 139 BY SIMILARITY.
FT CARBOHYD 138 138 N-LINKED (GLCNAC... ) (PROBABLE).
SQ SEQUENCE 459 AA; 53040 MW; 860B1A011AA47CF6 CRC64;

Query Match 34.7%; Score 938.5; DB 1; Length 459;
Best Local Similarity 38.5%; Pred. No. 2.4e-69;
Matches 189; Conservative 95; Mismatches 142; Indels 65; Gaps 8;

QY 35 KYNPLRPVANDSQPLTVYFSLSLQIMDVDEKNQVLTNNLQMSWTDHYLQWNVSEY 94
DB 10 ERYNKLIRPAVNSQQVTIGIKVSLAQILSVNERQIMTNWLTQETDRLWDPNEY 69

QY 95 PGKTVTRFPDQGIWKPDILLYNSADDERDATFHTNVLVNSGHCQYLPPIGFKSSCIDV 154
DB 70 EGIKKLRIPOSHIWLDPDIVLYNNADGVYEVSYFYNVAVNTGDIPLWPPAIYKSACATEV 129

QY 155 RWFFPDVQHCCLKFGWSYGGWSLDLQOE--ADISGYIPNGEMLVGIPOKRSRFFVEC 212
DB 130 RNFFPDQCNCTLKFRSWTYDRTDELVLTSDFASRDDYTPSGEWDIVSLPGRKNE----- 184

QY 213 CKEP-----YPDVTFVTWRRRTLYYGLNLLIPCVLISALALLVFLPADSGEKISLIGITV 268
DB 185 --DNNDLTLYDITDYFVIRKPLFTINLIIPCVLITSLAILVFLPSDCGEKVTLCMSV 242

QY 269 LLSLTTFMLVAEIMPATSDSVPLIAQVFASTMIIVGLSVVTVVILQVHHHDPDGGRMP 328
DB 243 LLALTVELLSKIVPPTSLAVPLIGKLMFTWLVTSIVTSVCVNLVHRSPTHTMP 302

QY 329 KWRVTVLLNWCAMFLRMKRPGEDEVKVRPACQHKQRCSLASVEMSAVAPPASNGNLLYIG 388
DB 303 EWKCVFLHKLPAFLMRPGRSNVRFRFRKQRKSPSSHQ----- 344

QY 389 FRGLDGVHCVTPDPSGVVCGRMACSPHDEHLLHGGQPPG-----DPDLAKIL 437
DB 345 -----DGDSFFLTDDPGRVCGAWRV-----GDLPEGSEFQRVKVRHQDQVDEAI 389

QY 438 EEVRYIANFRQDESEAVCSSEWKFACVDRCLCMAPSVFTIICTIGILMSAPNF----- 493
DB 390 DGVRFIAEHMKIEDDDDEGIIDWKYVAMVIDRLFWILVLCVCGVTGLGLFVQ-PLFQSN 448

QY 494 ---VEAVSKDF 501
DB 449 TPVAEEVYGVDF 459

```

SQ SEQUENCE 528 AA; 60675 MW; E76C6360AF876364 CRC64;
 Query Match 34.7%; Score 937.5; DB 1; Length 528;
 Best Local Similarity 37.8%; Pred. No. 3.4e-69;
 Matches 200; Conservative 85; Mismatches 175; Indels 69; Gaps 10;

Qy	8	WVAL-----AASLLHVSLSQGFORKLYKELVKNYNPLRPPVANDSQPIITVVFSLSLLOIMD 64
Dd	13	VWCFTVLQAATREQQKHGFAEDRLFKHLFTGYNWRSPVENTSDVVIVFGLSIAQLID 72
Qy	65	VDEKNOVLTTNIWLMSWTDHYLQNNVSEYPGVKTVFPDGQWKPKDILLVNSADRFDA 124
Dd	73	VDERQNMTTNIWLKLQEWSSDKURNPDEDNDVTSTIRVPSEMIIWDIPLYNNADGEFV 132
Qy	125	TFTNTLVNSSGHQCXYLPDPGIFKSSCVIDVRWFPPDVHQHKLFAGSMYSYGWSLDLMQE 184
Dd	133	THMTKAHLPSNGKVKKVPPAIYKSSCSIDVTYPFDQONCKMFGSWTYDKAKIDLNM 192
Qy	185	--ADISYIPNGEWDLVGIPGKSERPFYECKSGPYPDVTFVTVMRRRTLYYGNLLIPC 242
Dd	193	HHDVLDKYBESGEWAIIAIGRYNSKKYDCCTEIYPDITFYFVIRRLPLEFTINLIIPCL 252
Qy	243	LISALALLVPLLPADESKEKSLGITVLLSTTFTMLVAETMPATSDSVPIIAQYFASTMI 302
Dd	253	LISCLTVLVFLYSPDCGEKITLCISVLLSTVFLLLTITEIPSTLSVIPLIGYLLFTMI 312
Qy	303	IVGLSVVTVTLVQYHHDDGGCKMPKWTRVILLNWCAWFLMKR-----PGEDKV---- 353
Dd	313	FVTLSIIITVFLNVHRSPTTHPHWRSFFLGFTPRWLFMKRPPLLPABEGTTGOYD 372
Qy	354	RPACQHKQRCSLAS-----VEMSAVAPPASNGLLYIGFRGLDG 394
Dd	373	PPGTRLSTRCWLETVDVDDKWESEEEEEEEEEKAYPSRVPSG-----GSQG 424
Qy	395	VHCVPTPDSVCGRMACSPTHDEHLLHGQPPE---GD-----POLAKILEE 439
Dd	425	TQC-----HYSCEROAGKAS-----GGAPQVPLKGEEVGSDOGLTSPILRALEG 471
Qy	440	VRIANRRCODESEAVCSWKFACVDRCLCMASFVFTIICTIGILM 488
Dd	472	VQTIADHLRAEDADFQVEDDKWTKVAMVIDRIFLWMFIICLLGTGVGLF 520

RESULT 13
 ACH2 DROME
 ID _ACH2_DROME STANDARD; PRT; 576 AA.
 AC P17644; Q9VC73;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acetylcholine receptor protein, alpha-like chain 2 precursor.
 GN NACR-ALPHA-96AB OR ACNE OR SAD OR ACR96AB OR CG6844.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Prelygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head;
 RX MEDLINE=90301489; PubMed=2114015;
 RA Baumann A., Jonas P., Gundelfinger E.D.;
 RT "Sequence of D alpha 2, a novel alpha-like subunit of Drosophila
 RT nicotinic acetylcholine receptors.";
 RL Nucleic Acids Res. 18:3640-3640(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head;
 RX MEDLINE=90353591; PubMed=2117557;
 RA Jonas P., Baumann A., Merz B., Gundelfinger E.D.;
 RT "Structure and developmental expression of the D alpha 2 gene
 RT encoding a novel nicotinic acetylcholine receptor protein of
 RT Drosophila melanogaster."

RL FEBS Lett. 269:264-268(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90360975; PubMed=1697262;
 RA Sawruk E., Schloss P., Betz H., Schmitt B.;
 RT "Heterogeneity of Drosophila nicotinic acetylcholine receptors: SAD,
 RL EMBO J. 9:2671-2677(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=107311132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Agayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Balieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolehakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busan M.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
 RA de Fabros B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulo G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusker D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrtkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J., Yao Q.A.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: CNS IN EMBRYOS
 CC -!- DEVELOPMENTAL STAGE: LATE EMBRYONIC AND LATE PUPAL STAGES.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: X52274; CAA36517.1; --
 CC EMBL: X53583; CAA37652.1; --
 CC EMBL: AE003748; AAF56303.1; --
 CC PIR: S11679; ACFFA2.
 CC FlyBase: FBgn0000039; nAChR-alpha-96Ab.
 CC InterPro: IPR000188; GABAA_receptor.

DR InterPro: IPR001175; Neur_channel.
 DR Pfam: PF02931; Neur_chan_LBD; 1.
 DR Pfam: PF02932; Neur_chan_memb; 1.
 DR PRINTS: PR00252; NRIONCHANNEL.
 DR TRGFAMS: TRGR00860; LIC; 1.
 DR PROSITE: PS00236; NEUROTR_ION_CHANNEL; 1.
 KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 21 PROBABLE.
 FT CHAIN 22 576 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-
 FT DOMAIN 22 261 LIKE CHAIN 2. (POTENTIAL).
 FT TRANSMEM 262 285 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 293 311 POTENTIAL.
 FT TRANSMEM 327 346 POTENTIAL.
 FT DOMAIN 347 526 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 527 545 POTENTIAL.
 FT DISULFID 169 183 BY SIMILARITY.
 FT DISULFID 243 244 ASSOCIATED WITH RECEPTOR ACTIVATION
 FT CARBOHYD 65 65 (BY SIMILARITY).
 FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 570 570 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 576 AA; 65506 MW; 97D6A46CAD3F42F CRC64;
 Query Match 34.6%; Score 935.5; DB 1; Length 576;
 Best Local Similarity 38.1%; Pred No. 5.5e-69;
 Matches 203; Conservative 102; Mismatches 185; Indels 43; Gaps 9;
 Qy 3 CSPGVWLAALASLLHVSLOE-FQRLYKELVKNYNPLERPVANDSOPLTVYFSLSLQ 61
 Db 23 CKP--LCILLVLLLCETVQANPAKRLDYDLLSNYNRLRIRFVSNNTDTLVKGLRLSQ 80
 Qy 62 IMDVDKQVLTNNIWMQSWTDHYLQNVSEYSGVKTVPDPQGIWKPDIILLNSADER 121
 Db 81 LIDLNLKQILTTNWLEHEWQDHFKFWDPEYSGVTELYVPSEHIMLPDILVLYNADGE 140
 Qy 122 FDATFHTNVLNVSNGHCQYLPPIGFKSSCYIDVRFEPDVOHCKLFGSWSVGGWSDL- 180
 Db 141 YVVTMTKAILHYTGKVVVTPPAIFKSSCEIDVRFPPDQOTCFMKFGSWYDGGQIDLK 200
 Qy 181 ---QMQE-----ADISGYPNGEWDLVGIPGRSERFYECCKEYPDVTFTVMRRR 229
 Db 201 HISQNDKDNKVEIGIDREYVPSVEWDILGVAERHEKYYPCCAEPYPDIFFNILARK 260
 Qy 230 TLYYGLNLLIPCVLISALALVFLPADSGEKISLGITVLLSLTFTMLLVAEIMPATSDS 289
 Db 261 TLFYTNLIIPCVGISVLSVLVFLPADSGEKIALCISILLSQTMFFLLISEIIPSTSLA 320
 Qy 290 VPLIAQYFASPMIIVGLSVVTVIVLVQVHHHPDGGKMPKWTVRVILLNWCWFLMKRPG 349
 Db 321 LPLLGKYLFTMLLVGLSVITIIILNIHYRKPSTHKRPMRPIRSFFIKELPKLLMRVP- 379
 Qy 350 EDKVRPACQHKOR-----RCSLASVEMSAVAPPASNGNLL-YIGRGLDGVHC 397
 Db 380 KDLRLDLANKINYLKFSKTKFGQALMDENQMSGSSPSLRMQCRVGGGCGNHV 439
 Qy 398 VPTPD--SGVV-----CGRMACSPTHDEHLLHGGQPPGPDPAKILEEVRY 442
 Db 440 TTATNRFSGLVGALGGGLSTLSGNYGLPSVLSGLDSDLSVAAARKKYPFELEKATHVMF 499
 Qy 443 IANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTIICITIGILMSAPNFE 495
 Db 500 IQHEMQRODEFNAEDQDMGFVAMVMDRLFLWFLMIASLVGTGVILGEAPSLYD 552
 RESULT 14
 ACH4 CHICK
 ID ACH4 CHICK STANDARD; PRT; 622 AA.
 AC P09482;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE	Neuronal acetylcholine receptor protein, alpha-4 chain precursor.
OS	Gallus gallus (Chicken).
OC	Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
OC	Archosauia; Aves; Neognathae; Galliformes; Phasianidae; Oxyptila;
OC	Gallus.
OX	NCBI_TaxID=9031;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Brain;
RX	MEDLINE=88283624; PubMed=3267226;
RA	Nef P., Oneyver C., Alliod C., Couturier S., Ballivet M.;
RT	"Pentameric structure and subunit stoichiometry of a neuronal
RT	nicotinic acetylcholine receptor.";
RL	Nature 350:235-238(1991).
RN	[2]
RP	MUTAGENESIS OF GLU-289, AND SUBUNITS.
RX	MEDLINE=91172320; PubMed=2005979;
RA	Cooper E., Couturier S., Ballivet M.;
RT	"Pentameric structure and subunit stoichiometry of a neuronal
RT	nicotinic acetylcholine receptor.";
RL	Nature 350:235-238(1991).
CC	-I- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC	EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC	LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC	MEMBRANE.
CC	-I- SUBUNIT: NEURONAL ALPHA SEEMS TO BE COMPOSED OF TWO DIFFERENT
CC	TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (ALSO CALLED BETA). A
CC	FUNCTIONAL RECEPTOR SEEMS TO CONSIST OF TWO ALPHA-CHAINS AND
CC	THREE NON-ALPHA CHAINS.
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.
CC	-I- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC	-----
DR	ENBL; X07348; CAA30285.1; --
DR	ENBL; X07349; CAA30285.1; JOINED.
DR	ENBL; X07350; CAA30285.1; JOINED.
DR	ENBL; X07351; CAA30285.1; JOINED.
DR	ENBL; X07352; CAA30285.1; JOINED.
DR	ENBL; X07399; CAA30285.1; JOINED.
DR	ENBL; AJ250361; CAB59626.1; --
DR	PIR; S00379; ACCHAN.
DR	InterPro; IPR000188; GABAA receptor.
DR	InterPro; IPR001175; Neur Channel.
DR	Pfam; PF02931; Neur_chan_1BD; 1.
DR	Pfam; PF02932; Neur_chan_mem; 1.
DR	PRINTS; PR00252; NRIONCHANNEL.
DR	TIGRFAMS; TIGR00860; LIC; 1.
DR	PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW	Postsynaptic membrane; Ion channel; Glycoprotein; Signal;
KW	Transmembrane; Multigene family.
FT	SIGNAL
FT	CHAIN 1 223
FT	24 622
FT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
FT	ALPHA-4 CHAIN.
FT	EXTRACELLULAR.
FT	DOMAIN 24 237
FT	TRANSMEM 238 262
FT	TRANSMEM 270 288
FT	TRANSMEM 304 325
FT	DOMAIN 326 595
FT	TRANSMEM 596 614
FT	DISULFID 156 170
FT	DISULFID 220 221
FT	CYTOPLASMIC.
FT	BY SIMILARITY.
FT	(BY SIMILARITY)
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	E->K: REDUCES CHANNEL CONDUCTANCE BY
FT	HALF.
FT	HALF.

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OM protein - protein search, using sw model

Run on: June 20, 2003, 18:56:36 ; Search time 44 Seconds
(without alignments)
1096.806 Million cell updates/sec

Title: US-09-954-936-2

Perfect score: 2703

Sequence: 1 MRCSGGWLAALAHLS.....TIGILMSAPNFVEAVSKDFA 502

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2690	99.5	502	1 ACHUA7	nicotinic acetylch
2	2690	99.5	502	2 G02259	alpha 7 neuronal n
3	2545	94.2	502	2 A57175	nicotinic acetylch
4	2531	93.6	502	2 T01378	nicotinic receptor
5	2429	89.9	502	2 JN0113	nicotinic acetylch
6	1816.5	67.2	511	2 JH0173	alpha-bungarotoxin
7	1107.5	41.0	498	2 S68588	nicotinic acetylch
8	1089.5	40.3	560	2 T19822	hypothetical prote
9	998	36.9	461	2 T25671	hypothetical prote
10	947	35.0	557	2 S12359	nicotinic acetylch
11	944	34.9	542	2 T19862	hypothetical prote
12	942.5	34.9	511	2 A40110	nicotinic acetylch
13	938.5	34.7	459	2 S14703	nicotinic acetylch
14	937.5	34.7	528	1 ACCH2N	nicotinic acetylch
15	936.5	34.6	503	2 A53956	nicotinic acetylch
16	935.5	34.6	576	1 ACFFA2	nicotinic acetylch
17	934	34.6	622	1 ACCH4N	nicotinic acetylch
18	933	34.5	502	2 A37040	nicotinic acetylch
19	922	34.1	567	1 ACFFA1	nicotinic acetylch
20	916	33.9	627	2 JC4021	nicotinic acetylch
21	915.5	33.9	495	2 S60589	acetylcholine rece
22	913.5	33.8	625	2 A26456	nicotinic acetylch
23	912	33.7	495	2 B35721	nicotinic acetylch
24	898	33.2	494	2 T09289	probable nicotinic
25	895	33.1	517	2 A30992	nicotinic acetylch
26	887.5	32.8	499	2 A24572	nicotinic acetylch
27	884	32.7	498	2 G02421	nicotinic acetylch
28	877	32.4	521	1 ACFFNN	nicotinic acetylch
29	876.5	32.4	491	1 ACCHNN	nicotinic acetylch

30	876	32.4	470	2 A39218	nicotinic acetylch
31	874	32.3	512	2 B37014	nicotinic acetylch
32	861	31.9	502	2 S10505	nicotinic acetylch
33	857	31.7	457	2 S13872	nicotinic acetylch
34	850	31.4	457	2 A24383	nicotinic acetylch
35	849.5	31.4	511	2 T43634	nicotinic acetylch
36	848	31.4	445	2 I49458	acetylcholine rece
37	845	31.3	457	1 ACBOA1	nicotinic acetylch
38	844.5	31.2	500	2 S12899	nicotinic acetylch
39	842	31.2	457	1 ACHUA1	nicotinic acetylch
40	839	31.0	456	1 ACCHAN	nicotinic acetylch
41	838.5	31.0	503	2 JH0174	hypothetical prote
42	837.5	31.0	468	2 T24724	nicotinic acetylch
43	832.5	30.8	479	2 A53382	nicotinic acetylch
44	829.5	30.7	457	2 S08162	hypothetical prote
45	828	30.6	474	2 T27006	hypothetical prote

ALIGNMENTS

RESULT 1

ACHUA7

Nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - human
N:Alternate names: cholinergic nicotinate receptor alpha-7 chain
C:Species: Homo sapiens (man)
C:Date: 12-Aug-1996 #sequence revision 31-Jan-1997 #text_change 22-Jun-1999
C:Accession: I37185; A54194; S60309

R:Peng, X.; Katz, M.; Gerzanich, V.; Anand, R.; Lindstrom, J.

Mol. Pharmacol. 45, 546-554, 1994

A:Title: Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from the omers expressed in Xenopus oocytes.

A:Reference number: I37185; MUID:94195283; PMID:8145738

A:Accession: I37185

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-502 <PEN>

A:Cross-references: EMBL:X70297; NID:9496606; PIDN:CAA49778.1; PID:9496607

A:Experimental source: brain neuroblastoma cell line SHSY-5Y

R:Chini, B.; Raimond, E.; Elgoyhen, A.B.; Moralli, D.; Balzarotti, M.; Heinemann, S.

Genomics 19, 379-381, 1994

A:Title: Molecular cloning and chromosomal localization of the human alpha-7-nicotinic A:Reference number: A54194; MUID:94245214; PMID:8188270

A:Accession: A54194

A:Molecule type: mRNA

A:Residues: 24-363, 'S', 365-374, 'A', 376-408, 'AWPAP', 414-502 <CHI>

A:Cross-references: GB:Z23141; NID:9457736; PIDN:CAA80672.1; PID:9457737

A:Experimental source: retina

C:Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is localized C:Genetics:

A:Gene: GDB:CHRNA7

A:Cross-references: GDB:I38751; OMIM:118511

A:Map position: 15q14-15q14

A:Note: defects in this gene have been associated with mental retardation and schizophrenia C:Complex: the functional receptor molecule is a heteropentamer with two alpha chains a

C:Superfamily: acetylcholine receptor

C:Keywords: brain; glycoprotein; heteropentamer; ion channel; neurotransmitter receptor F:1-23/Domain: signal sequence #status predicted <Sig>

F:24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pred

F:231-254/Domain: transmembrane #status predicted <TR1>

F:262-280/Domain: transmembrane #status predicted <TR2>

F:296-317/Domain: transmembrane #status predicted <TR3>

F:470-488/Domain: transmembrane #status predicted <TR4>

F:46,90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:150-164/Disulfide bonds: #status predicted

F:365,413/Binding site: phosphate (Ser) (covalent) #status predicted

F:415/Binding site: phosphate (Thr) (covalent) #status predicted

F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match

Best Local Similarity 99.5%; Score 2690; DB 1; Length 502;

Matches 499; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRCSPGGWALAAASLLHVSLOGEFQRLKYELVKNYNPLERPVANDSQPLTVYFSL 60
 DB 1 MRCSPGGWALAAASLLHVSLOGEFQRLKYELVKNYNPLERPVANDSQPLTVYFSL 60
 QY 61 QIMDVDEKNOVLTTNIWLSWTDHYLQWNVSEYPGVKTFRPDGQIWKPDILLYNSADE 120
 DB 61 QIMDVDEKNOVLTTNIWLSWTDHYLQWNVSEYPGVKTFRPDGQIWKPDILLYNSADE 120
 QY 121 RFDPATFTNVLNVSNGHCQYLPFGIFKSSCYIDVRWPFDDVQHCCKLFGSWSYGGWSD 180
 DB 121 RFDPATFTNVLNVSNGHCQYLPFGIFKSSCYIDVRWPFDDVQHCCKLFGSWSYGGWSD 180
 QY 181 QMGEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPYDVFTVTMRRTLYYGLNLLIP 240
 DB 181 QMGEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPYDVFTVTMRRTLYYGLNLLIP 240
 QY 241 CVLISALALVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 DB 241 CVLISALALVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVTVIVLQYHHDDPGCKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
 DB 301 MIIVGLSVVTVIVLQYHHDDPGCKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
 QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 DB 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 QY 421 LHGGQPPGDPDLAKILEEVRYIANRFRQDESEAVSEWKFAACVVDRLCLMAFSVFTI 480
 DB 421 LHGGQPPGDPDLAKILEEVRYIANRFRQDESEAVSEWKFAACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 2

G02259
 alpha 7 neuronal nicotinic acetylcholine receptor - human
 C:Species: Homo sapiens (man)
 C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999
 C:Accession: G02259
 R:Leonard, S.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: H00936
 A:Accession: G02259
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-502 <LEO>
 A:Cross-references: EMBL:U40583; NID:g1125076; PIDN:AAA83561.1; PID:g1125077
 C:Superfamily: acetylcholine receptor

Query Match 99.5%; Score 2690; DB 2; Length 502;
 Best Local Similarity 99.4%; Pred. No. 3.4e-221;
 Matches 499; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRCSPGGWALAAASLLHVSLOGEFQRLKYELVKNYNPLERPVANDSQPLTVYFSL 60
 DB 1 MRCSPGGWALAAASLLHVSLOGEFQRLKYELVKNYNPLERPVANDSQPLTVYFSL 60
 QY 61 QIMDVDEKNOVLTTNIWLSWTDHYLQWNVSEYPGVKTFRPDGQIWKPDILLYNSADE 120
 DB 61 QIMDVDEKNOVLTTNIWLSWTDHYLQWNVSEYPGVKTFRPDGQIWKPDILLYNSADE 120
 QY 121 RFDPATFTNVLNVSNGHCQYLPFGIFKSSCYIDVRWPFDDVQHCCKLFGSWSYGGWSD 180
 DB 121 RFDPATFTNVLNVSNGHCQYLPFGIFKSSCYIDVRWPFDDVQHCCKLFGSWSYGGWSD 180
 QY 181 QMGEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPYDVFTVTMRRTLYYGLNLLIP 240
 DB 181 QMGEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPYDVFTVTMRRTLYYGLNLLIP 240

QY 241 CVLISALALVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 DB 241 CVLISALALVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVTVIVLQYHHDDPGCKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
 DB 301 MIIVGLSVVTVIVLQYHHDDPGCKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
 QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 DB 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 QY 421 LHGGQPPGDPDLAKILEEVRYIANRFRQDESEAVSEWKFAACVVDRLCLMAFSVFTI 480
 DB 421 LHGGQPPGDPDLAKILEEVRYIANRFRQDESEAVSEWKFAACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 3

A57175
 nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 20-Aug-1999
 C:Accession: A57175
 R:Orr-Urtreger, A.; Seldin, M.F.; Baldini, A.; Beaudet, A.L.
 Genomics 26, 399-402, 1995
 A:Title: Cloning and mapping of the mouse alpha7-neuronal nicotinic acetylcholine receptor
 A:Reference number: A57175; MUID:95324936; PMID:7601470
 A:Accession: A57175
 A:Status: preliminary
 A:Molecule type: mRNA

A:Residues: 1-502 <ORR>
 A:Cross-references: GB:L37663; NID:g790853; PIDN:AAC42053.1; PID:g790854
 C:Superfamily: acetylcholine receptor
 C:Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprotein
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status predicted
 F:231-254/Domain: transmembrane #status predicted <TR1>
 F:262-280/Domain: transmembrane #status predicted <TR2>
 F:296-317/Domain: transmembrane #status predicted <TR3>
 F:470-488/Domain: transmembrane #status predicted <TR4>
 F:46,90,133/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:365,413,427/Binding site: phosphate (Ser) (covalent) #status predicted
 F:415/Binding site: phosphate (Thr) (covalent) #status predicted
 F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 94.2%; Score 2545; DB 2; Length 502;
 Best Local Similarity 93.8%; Pred. No. 7.8e-209;
 Matches 466; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 6 GGWMLAALASLLHVSLOGEFQRLKYELVKNYNPLERPVANDSQPLTVYFSL 65
 DB 6 GGWMLAALASLLHVSLOGEFQRLKYELVKNYNPLERPVANDSQPLTVYFSL 65
 QY 66 DEKNOVLTTNIWLSWTDHYLQWNVSEYPGVKTFRPDGQIWKPDILLYNSADERF 125
 DB 66 DEKNOVLTTNIWLSWTDHYLQWNVSEYPGVKTFRPDGQIWKPDILLYNSADERF 125
 QY 126 FHTNVLNVSNGHCQYLPFGIFKSSCYIDVRWPFDDVQHCCKLFGSWSYGGWSD 185
 DB 126 FHTNVLNVSNGHCQYLPFGIFKSSCYIDVRWPFDDVQHCCKLFGSWSYGGWSD 185
 QY 186 DISGYIPNGEWDLVGIPGKRSEFYECCKEYPYDVFTVTMRRTLYYGLNLLIP 245
 DB 186 DISGYIPNGEWDLVGIPGKRSEFYECCKEYPYDVFTVTMRRTLYYGLNLLIP 245
 QY 246 ALALVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 305
 DB 246 ALALVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 305

QY LSVVTVTVLYLQVHHHDPDGGKMPKMTWVILLNCAFLMRKRGEDKVRPAQCHKORCS 365
Db LSVVTVTVLYLRHHHPDGGKMPKMTWVILLNCAFLMRKRGEDKVRPAQCHKPARCS 365
QY LSVVEMSAVAPPPASNGNLLTYGFRGLDGVHCVPTPDGSGVCCRMACSPPHDEHLHGQ 425
Db LMSVELLSAAGPPTSGNLLTYGFRLEGNHCAPTPDGSVCCRLACSPHDEHLHGTH 425
QY PEEGDEDLAKILEEVYIINRFRCODESEAVSEMKFAACVVDRLCLMAFSVTLICTIG 485
Db PEGDEDLAKILEEVYIINRFRCODESEVTCSEMKFAACVVDRLCLMAFSVTLICTIG 485
QY ILSAPNFEVAVSKDFA 502
Db ILSAPNFEVAVSKDFA 502

RESULT 4
T01378
nicotinic receptor alpha 7 chain - rat
C.Species: Rattus norvegicus (Norway rat)
C.Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000
C.Accession: T01378
R.Seguel, P.; Madiche, J.; Dineley-Willer, K.; Dani, J.A.; Patrick, J.W.
J.Neurosci. 13, 596-604, 1993
A.Title: Molecular cloning, functional properties, and distribution of rat brain alpha
A.Reference number: Z14310; M0ID:93147931; PMID:7678857
A.Accession: T01378
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-502 <SEG>
A.Cross-References: EMBL:S53987; NID:G264770; PIDN:AA25224.2; PID:95705903
A.Experimental source: brain
C.Superfamily: acetylcholine receptor

Query Match	93.6%;	Score 2531;	DB 2;	Length 502;
Best Local Similarity	93.4%;	Pred. No. 1.2e-207;		
Matches 464; Conservative	18;	Mismatches 15;	Indels 0;	Gaps 0;

Qy	6	GGVMTALASLHVSLQGFQRLCYKELYKYNVPLRPVANDSOPLTVYSLSLQIMDV	65
Db	6	GGIWTALAAALHVSLQGFQRLCYKELYKYNVPLRPVANDSOPLTVYSLSLQIMDV	65
Qy	66	DEKNOVLTTNIWLOMSWTDHYLQMNVSXYPGVKTARFPDGOIWKPDILLYNSADERPDAT	125
Db	66	DEKNOVLTTNIWLOMSWTDHYLQMNVSXYPGVKNVAFPDGOIWKPDILLYNSADERPDAT	125
Qy	126	FHTNVLVNSSGHCQIYLPFGIFKSSCTIYDRWPFDFYQHCYKFKGSMVSGGMSLDLOMOEA	185
Db	126	FHTNVLVNASGHCQIYLPFGIFKSSCYIDRWPFDFYQOQCKLKGSMSVSGMSLDLOMOEA	185
Qy	186	DISGYIPNEMWLVGIPGAKSEREFYECCKEYPDVFVTVMRRRTLYYGNTLIIPCVLIS	245
Db	186	DSSYIIPNEMWLVGIPGAKRNEKFYECCKEYPDVFVTVMRRRTLYYGNTLIIPCVLIS	245
Qy	246	ALALVFLPLPADSGEKISLGIITVLSLSTFMILVAEIMPATSDSVPLIAQYFASMTIIVG	305
Db	246	ALALVFLPLPADSGEKISLGIITVLSLSTFMILVAIMPATSDSVPLIAQYFASMTIIVG	305
Qy	306	LSVVTVTVIYLQYHHNDPDGCKMPKMTRVILILMWCAFLRMKRPGEDEVKRPACOHKORCS	365
Db	306	LSVVTVTVILRHHNDPDGCKMPKMTRIILILMWCAFLRMKRPGEDEVKRPACOHKPRCS	365
Qy	366	LASVMSAVAPRPASNGNLIYIGFREGDQVHCVPYRDSGVYGRMDCSPYHNDHLLHGGQ	425
Db	366	LASVLSISAGAPRPTSNGNLIYIGFRLBEMHCAPYRDSGVYCGRLCSPYHNDHLLHMGAR	425
Qy	426	PPEGDPDLAKILIEEYRYIINRPRCODESEAVCSSEWKFPAACVVDRLCILMAFSVYTIICTIG	485
Db	426	PSDGPDPDLAKILIEEYRYIINRNRCCODESEVICSEWKFPAACVVDPLCLMAFSVYTIICTIG	485
Qy	486	ILMSAPNFEAVSXDPA 502	

Db 486 ILMAPNFVEAVSKDEFA 502

RESULT 5

nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - chicken
N;Alternate names: alpha-bungarotoxin-binding protein alpha chain

```
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Aug-1999
```

R; Couturier, S.; Bertrand, D.; Matter, J.M.; Hernan-

A; Title: A neuronal nicotinic acetylcholine receptor subunit

A;Accession: JN0113

A;Residues: 1-502 <COU>

A; Experimental source:

Neuron 5, 35-48, 1990

A:Reference number: JH0172; MUID:90315158; PMID:2369519

A;Molecule type: mRNA

A; Cross-references: EMB

R;Matter-Sadzinski, L.;
A;Experimental source:

EMBO U. 11, 4523-4538,
A;Title: Neuronal speci

A;Accession: S28018

```
A;Residues: 1-18 <MAS>
A;Molecule type: DNA
```

A;Experimental source:

R. COLLIER-HOON, B.M.;
Proc. Natl. Acad. Sci.

A;Reference number: A94

A;Accession: B25/38
A:Molecule type: protei

C;Comment: This acetyl

A: Introns: 19/1: 65/3:

C:Keywords: brain: glyco

```
F:1-23/Domain: signal s
F:24-502/Product: nicot
```

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F:231-254/Domain: trans
F:262-280/Domain: trans
```

F:470-488/Domain: trans

F;46,90,133/Binding site
F;365,367,413,427,465/B

F:442/Binding site: pho

Query Match

Best Local Similarity
Matches 449: Conserved

8 VWT.A1.AAST.

Dh 8 TWTAAAGT

68 KNOWT, TTN, T

68 KNOVT.TTN.TT

128 TNYT.VNSSG

[illegible]

Db 128 TNVLNSSGHCQYLPPIGKSSCYIDVRWPFDFVQKCNLKFSGSWTYCGNSLDLQMOEADI 187
Qy 188 SGVINGEWDLVGIPIGKRSEFVECCKEPDPVDTFTVTRRRRTLYYGLNLLIPCVLISAL 247
Db 188 SGVINGEWDLVGIPIGKRSEFVECCKEPDPDTFTVTRRRRTLYYGLNLLIPCVLISAL 247
Qy 248 ALLVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASFTMIIVGLS 307
Db 248 ALLVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASFTMIIVGLS 307
Qy 308 VVTVIVLYQHHHDPDGGKMPKWRVILLNWCWFLRMKRPBGDKVRPACQHKQRCSLA 367
Db 308 VVTVIVLYQHHHDPDGGKMPKWRVILLNWCWFLRMKRPBGDKVRPACQHKQRCSLA 367
Qy 368 SVEMSAVAPPASNGNLLYIGFGLDGVHCVPTPDSGVCGRMACSTHDEHLLHGQOPP 427
Db 368 SVEMSAVAPPASNGNLLYIGFGLDGVHCVPTPDSGVCGRMACSTHDEHLLHGQOPP 427
Qy 428 EGDPDLAKILEEVRYIANRPRCODESEAVCESEWKFACVVDRLCLMAFVSFTIICIGIL 487
Db 428 EGDPDLAKILEEVRYIANRPRCODESEAVCESEWKFACVVDRLCLMAFVSFTIICIGIL 487
Qy 488 MSAPNFVEAVSKDFA 502
Db 488 MSAPNFVEAVSKDFA 502

RESULT 6
JH0173
A:Species: Gallus gallus (chicken)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Aug-1999
C:Accession: JH0173
R:Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.
Neuron 5, 35-48, 1990
A:Title: Brain alpha-bungarotoxin binding protein cDNAs and Mabs reveal subtypes of this
A:Reference number: JH0172; MUID:90315158; PMID:2369519
A:Accession: JH0173
A:Molecule type: mRNA
A:Residues: 1-511 <SCH>
A:Cross-references: GB:X52296; NID:g63081; PIDN:CAA36544.1; PID:g63082
A:Experimental source: brain
A:Note: this sequence is similar to acetylcholine receptor alpha chains
C:Comment: Alpha-bungarotoxin binding proteins are localized to extrasynaptic pseudodend
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; transmembrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-510/Product: alpha-bungarotoxin binding protein alpha-2 chain #status predicted <AE
F:239-262/Domain: transmembrane #status predicted <TM1>
F:270-288/Domain: transmembrane #status predicted <TM2>
F:304-323/Domain: transmembrane #status predicted <TM3>
F:479-496/Domain: transmembrane #status predicted <TM4>
F:54/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 67.2%; Score 1816.5; DB 2; Length 511;
Best Local Similarity 68.8%; Pred. No. 9.5e-147;
Matches 342; Conservative 56; Mismatches 94; Indels 5; Gaps 4;
Qy 8 VMLAASLLHVSLOGEFQRLKLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMDVDE 67
Db 16 LWASLFLSPFKVQCGESQRLYDLRNYNRLERPVANDSQPIVLEQLSLQIIDVDE 75
Qy 68 KNQVLTNIWLQMSWTDHYLQWNVSEYPGVKTVRFPDQGIWKPDILLYNASADERFDATFH 127
Db 76 KNQVLTNIWLQMSWTDHYLQWNVSEYPGVKTVRFPDQGIWKPDILLYNASADERFDATFH 135
Qy 128 TNVLNSSGHCQYLPPIGKSSCYIDVRWPFDFVQKCNLKFSGSWTYCGNSLDLQMOEADI 187
Db 136 TNVLNYSVCQYIPPGILKSTCYIDVRWPFDFVQKCNLKFSGSWTYCGNSLDLQMOEADI 195
Qy 188 SGVINGEWDLVGIPIGKRSEFVECCKEPDPVDTFTVTRRRRTLYYGLNLLIPCVLISAL 247

Db 196 SNYISNGEWDLVGPGRKNELYYECCKEPDPVDTFTVTRRRRTLYYGLNLLIPCVLISGL 255
Qy 248 ALLVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASFTMIIVGLS 307
Db 256 ALLVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASFTMIIVGLS 315
Qy 308 VVTVIVLYQHHHDPDGGKMPKWRVILLNWCWFLRMKRPBGDKVRPACQHK--QRRK 364
Db 316 VVTVIVLYQHHHDPDGGKMPKWRVILLNWCWFLRMKRPBGDKVRPACQHK--QRRK 374
Qy 365 SLASVENSAPAPPASNGNLLYIGFGLDGVHCVPTPDSGVCGRMACSTHDEHLLHG 424
Db 375 SLKNTENMLVPGHQPSNGNMIY-SYHTMENPCCQNNDLGSKSGKITCPLSEDMEHVQKK 433
Qy 425 QPEGDPDLAKILEEVRYIANRPRCODESEAVCESEWKFACVVDRLCLMAFVSFTIIC 484
Db 434 ALMDTIVIVKILEVOFIAMRFKQDEGEIASEWKFACVVDRLCLMAFVSFTIIC 493
Qy 485 GILMSAPNFVEAVSKDF 501
Db 494 TILMSAPNFVEAVSKDF 510

RESULT 7
S68588
nicotinic acetylcholine receptor alpha-1 chain precursor (clone Ce21) - Caenorhabditis
C:Species: Caenorhabditis elegans
C:Date: 06-Dec-1996 #sequence_revision 07-Feb-1997 #text_change 20-Aug-1999
C:Accession: S68588; S57496
R:Ballivet, M.; Alliod, C.; Bertrand, S.; Bertrand, D.
J. Mol. Biol. 258, 261-269, 1996
A:Title: Nicotinic acetylcholine receptors in the nematode Caenorhabditis elegans.
A:Reference number: S68587; MUID:96196478; PMID:8627624
A:Accession: S68588
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-498 <BAL>
A:Cross-references: EMBL:X83887; NID:g872087; PIDN:CAA58764.1; PID:g872088
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-498/Product: nicotinic acetylcholine receptor alpha-1 chain #status predicted <MAT

Query Match 41.0%; Score 1107.5; DB 2; Length 498;
Best Local Similarity 44.6%; Pred. No. 2.4e-86;
Matches 226; Conservative 77; Mismatches 167; Indels 37; Gaps 7;
Qy 10 LALAASLLHVSLOGEFQRLKLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMDVDEK 68
Db 6 LLISCAILLAAPTLGSLOERRLYDLMRNYYNLERPVANHSEPVTVHLKVALQIIDVDEK 65
Qy 69 NQVLTNIWLQMSWTDHYLQWNVSEYPGVKTVRFPDQGIWKPDILLYNASADERFDATFH 128
Db 66 NQVTVVNAWLDYTWNDYNLVMDKAEYGNITDVRFPAGKIMKPDVLLNVSDTNFDSTYQT 125
Qy 129 NVLYNSSGHCQYLPPIGKSSCYIDVRWPFDFVQKCNLKFSGSWTYCGNSLDLQMOEA--D 186
Db 126 NMIVYSTGLVHWVPPGIFKISCKIDIQWFPDEQKCFKFGSWTYDGYKLDQAPATGDFD 185
Qy 187 ISGYIPNGEWDLVGIPIGKRSEFVECCKEPDPVDTFTVTRRRRTLYYGLNLLIPCVLISA 246
Db 186 ISEYISNGEWALPLTTVERNEKFDCCPEPVDVHFVLMRRRTLYYGLNLLIPCVLISA 245
Qy 247 LALLVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASFTMIIVGL 306
Db 246 MTLGFTLPPDAGEKITLQITVLLSICPFLSIVSEMSPTSEAVPFLGIFFTCCMIVVTA 305
Qy 307 SVVTVIVLYQHHHDPDGGKMPKWRVILLNWCWFLRMKRPBGDKVRPACQHKQRCSL 366
Db 306 STVFTVYVNLNHYRTPETHDMPTRNLLYWIPIMLRMKRPG-----HNLTYSAL 356
Qy 367 ASVEMSAVAPPASNGNLLYIGFGLDGVHCVPTPDS-----GVVCGRMAC 412

Db 357 PSL-----FSTKPNRHSLSIRNIK--DNEHSLSRANSFPDADCLRLNQYIMTQSVNSGLTSL 410
Qy 413 SPFHDEHLLHGGQPPGDPD-----LAKILEEYVYIANRFRQDESEAVCSWEKFAACVW 467
Db 411 GSIPSTMISSNGTTTDSVQOATLLIHLRIYHELKIVTKRMTEGDKKEQACNNKWKFAAMV 470
Qy 468 DRCLMAFSPFTTICTIGILMSAPNV 494
Db 471 DRCLVYFTTIFIVSTIGIFWSAPYLV 497

RESULT 8
T19622
hypothetical protein C31H5.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T19622
R:Kershaw, J.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: T19622
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-560 <WIL>
A:Cross-references: EMBL:Z93778; PIDN: CAB07843.1; GSPDB: GNO0019; CESP: C31H5.3
A:Experimental source: Clone C31H5
C:Genetics:
A:Gene: CESP: C31H5.3
A:Map position: 1
A:Introns: 24/1; 70/3; 139/2; 270/1; 299/1; 336/3; 372/2; 456/3
C:Superfamily: acetylcholine receptor

Query Match 40.3%; Score 1089.5; DB 2; Length 560;
Best Local Similarity 40.6%; Pred. No. 9.5e-85;
Matches 226; Conservative 93; Mismatches 157; Indels 81; Gaps 9;

Qy 10 LALAASLL-----HVSLOGERQKLYKELVKNYNPLRPVANDSQPLTVYFSLSLQI 62
Db 8 LVLVSILIWETKCSKVITWGDHERRLYAKLAENYNKLARPVNESEAVVLLGMDYQOI 67
Qy 63 MDVDERNOVLTITNWLQMSWTDHYLQWNVSEYGVKTVRPDPGQIWKPDILLVNSADERF 122
Db 68 LDIDEXHQIMNSVNLWLSMTDHYLTWDPSEFGNKEVRLPINNWKPDILLVNSVDPQOF 127
Qy 123 DATFTFNVLNVSCHQYLPPIGFKSCYIDVRWFFDVQHCCLKFGSWSYGVGSLDQW 182
Db 128 DSTWPNVAVLYTGNVTWIPALIRSCAIDIAFPDTHCTWKFSGWTYSGEFTDLIN 187
Qy 183 QEADISGYIPNGEWDLVGIPGKRSEFYCKPEYDPDVTFTVMRRRTLYYGLNLLIPCV 242
Db 188 TTISPATYKPNGEWELLGLTSQRSIFFEYCCPEYDVTFTVSIRRTLYYGFNLLPCM 247
Qy 243 LISALALLVFLPADSGEKISLIGITVLLSTTMMLLVAEIMPATSDSVPLIAQYFASTMI 302
Db 248 LISSALLSFTLPADCGEKLNGVTIFMSLCVFEMVAAEMPQTSALPLIQIFYSCIMF 307
Qy 303 IYGLSVVTVTVILQYHHHDPDGGK-MPKWTRVILLANWCAMFLMKRPGEDKVRPACOH-- 359
Db 308 QVGSVAIVTIALNFHRRSPEQYKPNKFKLTKLLGLLPTLLGMERPDVLELSVHGAYHA 367
Qy 360 ----KORRCSLASVEMSAVAPPASNGNLLIYIGRGLD----- 393
Db 368 SDNKKQYQYLLVEVERHILTRP---NGN-----GHSADVAKAVHLDLSTGNPHSDAKSSPS 420
Qy 394 -----GVHCVPPT-----DSGV---VCGRMACSPTHDEHLLHGGQPPGDPD--- 431
Db 421 PKRTSASIMGMTGLPTTQMNGALDSSINKYCTKTVRPLENGSATINHKSSPOINPINN 480
Qy 432 -----DLAKILEEYVYIANRFRQDESEAVCSWEKFAACVDRCLCLMAP 475
Db 481 NTKCANNOKTQFEDRHHILNELRVISARVKEEAMHALQADWMPASRVDRVCFLAF 540
Qy 476 SVFTTICTIGILMSAPN 492

Db 541 SAFLPFXCTAISYNAPH 557

RESULT 9
T25671
hypothetical protein D2092.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T25671
R:Gattung, S.; Maggi, L.
submitted to the EMBL Data Library, February 1997
A:Description: The sequence of C. elegans cosmid D2092.
A:Reference number: Z20067
A:Accession: T25671
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-461 <GAT>
A:Cross-references: EMBL:U88167; PIDN: AAB42223.1; GSPDB: GNO0019; CESP: D2092.3
A:Experimental source: strain Bristol N2; clone D2092
C:Genetics:
A:Gene: CESP: D2092.3
A:Map position: 1
A:Introns: 36/1; 80/3; 119/2; 191/1; 243/1; 274/1; 303/1; 382/2
C:Superfamily: acetylcholine receptor

Query Match 36.9%; Score 998; DB 2; Length 461;
Best Local Similarity 39.8%; Pred. No. 4.6e-77;
Matches 197; Conservative 96; Mismatches 146; Indels 56; Gaps 8;

Qy 12 LAASLLHVSL--QGEF--QRKLYKELVKNYNPLRPVANDSQPLTVYFSLSLQIMVDENK 69
Db 10 LSLVIIHSNLCGSAETKLTDLKLGYNPLRPVQNSSQPLEVKIKLFLQQLDLDVENK 69
Qy 70 QVLTNTNLQMSWTDHYLQWNVSEYGVKTVRFP--DQIWKPDILLVNSADERDAPFH 127
Db 70 QIVSNWALSYTWFTHKLQWEPKYGIGQIRFFGSSDHIWKPDILLVNSAEDFDSTFK 129
Qy 128 TNVLNVSCHQYLPPIGFKSCYIDVRWFFDVQHCCLKFGSWSYGVGSLDQW---- 182
Db 130 SNLTYHTGTWVPPGVKVCQLDVTWFFDDQVCEMKFGSWTFHGYAIDLQIDDDTN 189
Qy 183 --QEADISGYIPNGEWDLVGIPGKRSEFYCKPEYDPDVTFTVMRRRTLYYGLNLLIP 240
Db 190 GTQSMDLSTLVNGEWQVISTNAKRVSYKKCCPEYTVNYLHRRRTLYYGFNLLIP 249
Qy 241 CVLISALALLVFLPADSGEKISLIGITVLLSTTMMLLVAEIMPATSDSVPLIAQYFAST 300
Db 250 SLLISLMAILGFMFPDAGEKITLEVITLLAIVFSLMSVSEMTPTSEAVPLIGVFFSCC 309
Qy 301 MIIVGLSVVTVTVILQYHHHDPDGGKMPKWTRVILLANWCAMFLMKRPGEDKVRPACQHK 360
Db 310 MLVVSASVFTVIVNLNLFHSADSHENMPLVRRVLLLEFLPMLFMSRPGYKFKV-- 363
Qy 361 -QRRCSLASVEMSAVAPPASNGNLLIYIGRGLDGVHCV-TPDSGVVCGRMACSPTHDEH 419
Db 364 -----ANV-----IDSTDMKPKPKPLDCLNLPNSNHAGYEAQ 395
Qy 420 LLHGGQPPGDPDLAKILEEYVYIANRFRQDESEAVCSWEKFAACVVDRLCLMAFSVFT 479
Db 396 ILL-----LHSVHTELRRVVAFYFNKEEHERIQTDWRFAAMVVDRACLLLFTVFI 445
Qy 480 ICTIGILMSAPNV 494
Db 446 VISILAIMSAPHII 460

RESULT 10
S12359
nicotinic acetylcholine receptor alpha-L1 chain precursor - desert locust
C:Species: Schistocerca gregaria (desert locust)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C:Accession: S12359

R;Marshall, J.; Buckingham, S.D.; Shingai, R.; Lunt, G.G.; Goosey, M.W.; Darlison, M.G.; EMBO J. 9, 4391-4398, 1990
A;Title: Sequence and functional expression of a single alpha subunit of an insect nicotinic acetylcholine receptor
A;Reference number: S12359; MUID:91092263; PMID:1702381
A;Accession: S12359
A;Molecule type: mRNA
A;Residues: 1-557 <MAR>
A;Cross-references: EMBL:X55439; NID:g10133; PIDN:CAA39081.1; PID:g10134
C;Superfamily: acetylcholine receptor
C;Keywords: glycoprotein; ion channel; neurotransmitter receptor; transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-557/Product: nicotinic acetylcholine receptor alpha-L1 chain #status predicted <MAT>
F;245-266/Domain: transmembrane #status predicted <TM1>
F;274-295/Domain: transmembrane #status predicted <TM2>
F;308-329/Domain: transmembrane #status predicted <TM3>
F;501-523/Domain: transmembrane #status predicted <TM4>
F;47,235/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 35.0%; Score 947; DB 2; Length 557;
Best Local Similarity 37.1%; Pred. No. 1.3e-72;
Matches 201; Conservative 92; Mismatches 177; Indels 72; Gaps 6;

QY 5 PGGWALAAALHVSLOGEFQRLKYLKVNTPNPLRPVANDSQPLTVYFSLSLQIMD 64
Db 6 PMLLLLLLLLHHPAAANPDARLYDLSNRYLRIPVSNNTDTVLVXGLRLSLQID 65
QY 65 VDEKNQVLTTNIWQSWTDHYLQNVSEYGVKTVRFPDQIWKPDILLYNSADERFDA 124
Db 66 LNKQQLTTNVLEHWDHQRWDPAEYGGVTELYVPSSEHILWPDVLVNNADGEYV 125
QY 125 THTNVLNVSNGHCOYLPPGIFKSSCYIDVRFPPFVQHCXKLPFGSNGWSLDQ--- 181
Db 126 TMTKAVLHHTGKVVWTPPAIFKSSCEIDVRYFPFDDQTCFMKFGSWTYDGDQIDLKH 185
QY 182 -----MQEADISGYIPNGEWDLVGIPGKRSERFVECKEPPDVTFTVMRRRLYY 233
Db 186 QKYDDNKVKVIGIDIREYPSVWEVDILGVAERHEKYPCCAEYPDIFFTILTRKTLFY 245
QY 234 GLNLLIPCVLISALALVFLPADSGEKISIGITVLISLTFTMLLVAEIMPATSDSVPLI 293
Db 246 TVNLIVPCVGISLVSLVFLPADSGEKIALCISILLSQTMFFLLSEIIPSTSLAFLPL 305
QY 294 AQYFASTMIIVGLSVVTVIVLQYHHHPDGGKMPKTRVILLNWCWFLRMKPEGE--- 350
Db 306 GKYLFTMLVGLSVITIVLVNHYKPKTHKAPVWRKVFIRRLKLLMRVPEQLLA 365
QY 351 DKVRPAQKHQRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVCHVPTPDGSGVWCGRM 410
Db 366 DLASKRLRLRAHNSKLSAAAAAATAAASSS-----AASSPDS--LRHH 408
QY 411 ACSPTHDEHL-LHGGQPEG----- 429
Db 409 LHQHQHQLHLQLHLQRPGGCNGLHSATNRFPGSAGAFGGLPSVVGSLGSLDVATRK 468
QY 430 DPDLKILEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTIICIGILMS 489
Db 469 PFELEKAIHNVLFIONHQKQDEDAEDQDQMGFVAMVDRDLFLWIFTIASIVGTAILCE 528
QY 490 AP 491
Db 529 AP 530

RESULT 11
T19862
hypothetical protein C40C9.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T19862
R;Hemby, C.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19188
A;Accession: T19862

A;Status: preliminary; translated from GB/EMBL/DBDJB
A;Molecule type: DNA
A;Residues: 1-542 <WIL>
A;Cross-references: EMBL:Z70266; PIDN:CAA94206.1; GSPDB:GN00028; CESP:C40C9.2
A;Experimental source: clone C40C9
C;Genetics:
A;Gene: CESP:C40C9.2
A;Map position: X
A;Introns: 11/3; 69/3; 123/3; 216/1; 248/1; 279/1; 314/1; 350/3; 430/1; 464/1; 4
C;Superfamily: acetylcholine receptor

Query Match 34.9%; Score 944; DB 2; Length 542;
Best Local Similarity 37.7%; Pred. No. 2.3e-72;
Matches 207; Conservative 93; Mismatches 165; Indels 84; Gaps 15;

QY 11 ALAASLLHV-----SLOGEFQRLKYLKVNTPNPLRPVANDSQPLTVYFSLSLQIMDV 65
Db 12 ALHCVLFHLLTEVHSSADEY--RLADLRHNDYRPPVAVASEPLVSVKYYLQQLIDV 69
QY 66 DEKNQVLTTNIWQSWTDHYLQNVSEYGVKTVRFPD--GQIWKPDILLYNSADERFD 123
Db 70 DEKNQVITLVAMIEYQWTDYKWKWDPSYGGIKDIRIPGNANAIWKPDVLLYNSADENFD 129
QY 124 ATHTNVLNVSNGHCOYLPPGIFKSSCYIDVRFPPFVQHCXKLPFGSNGWSLDQIM- 182
Db 130 STYPNVVWSYTGVDVLQVPPGILKLSCKIDITYFPDDQICHLKFGSWTSGNFIDLRIN 189
QY 183 -----QEADISGYIPNGEWDLVGIPGKRSERFVECKEPPDVTFTVMRRRLYY 233
Db 190 GPEGKNSDEGIDVOYVQNGEWLLAVPARHETNIFD--EOPYPSLFFYLIHQRTLYY 247
QY 234 GLNLLIPCVLISALALVFLPADSGEKISIGITVLISLTFTMLLVAEIMPATSDSVPLI 293
Db 248 GLNLLIPFSLISLTMTVLGFTLPPDAGEKITLITLISVCFELSNVADMTPTSEAVPLI 307
QY 294 -----AQYFASTMIIVGLSVVTVIVLQYHHHPDGGKMPKTRVILLNWCWFLRMKR 347
Db 308 GLIIFSGAFFSCCLLVWSASVVFVTLVNLNHRKPETHMSPFLRELLLIWLPMLLMRR 367
QY 348 PGEKVRPAQKHQRCSLASVEMSAVAPPASNGNLLYIG-FRGLDGVCHVPTPDGSG--- 404
Db 368 PG--KTIIFNCTPLHKAEEKAKOGSI-----KNG-----VGPGRKPTDSVH---PSEGLS 412
QY 405 -----VVCGR-MACSPTHDEHLHGG-----QPEGDP----- 431
Db 413 LMKNIKLRQOTIDFEYEFHVOHNLMPVASEMTPRTVYSKVAESVEDVVMTELK 472
QY 432 -----DLAKILEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTIICIG 485
Db 473 MQKACLELKNISSQTRAMRKKEEDEDEQAANDWKFAAMVVDRCCLITFSFVIVSTCG 532
QY 486 ILMGAPNFV 494
Db 533 IMFSSPHLI 541

RESULT 12
A40110
nicotinic acetylcholine receptor alpha-2 chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Mar-1992 #sequence_revision 10-Apr-1992 #text_change 20-Aug-1999
C;Accession: A40110
R;Wada, K.; Ballivet, M.; Boulter, J.; Connolly, J.; Wada, E.; Deneris, E.S.; Swanson,
Science 240, 330-334, 1988
A;Title: Functional expression of a new pharmacological subtype of brain nicotinic acetylcholine receptor
A;Reference number: A40110; MUID:88178113; PMID:2832952
A;Accession: A40110
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-511 <WAD>
A;Cross-references: GB:M20297; NID:g202672; PIDN:AAA40664.1; PID:g202674
A;Note: the authors translated the codon TCG for residue 494 as Cys
C;Superfamily: acetylcholine receptor

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: Jun 20, 2003, 19:00:32 ; Search time 52 Seconds
(without alignments)
1044.612 Million cell updates/sec

Title: US-09-954-936-2
Perfect score: 2703
Sequence: 1 MRCSPGVWLALAAASLLHVS.....TIGILMSAPNFVEAVSKDFA 502

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pdb.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pdb.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pdb.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pdb.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pdb.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pdb.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pdb.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pdb.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pdb.*
10: /cgn2_6/ptodata/2/pubpaa/US05_PUBCOMB.pdb.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pdb.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pdb.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pdb.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2703	100.0	502	9	US-09-954-936-2
2	2698	99.8	502	10	US-09-892-985-8
3	1254.5	46.4	501	10	US-09-303-232-6
4	1242	45.9	496	10	US-09-303-232-4
5	1155.5	42.7	770	10	US-09-303-232-2
6	959	35.5	622	10	US-09-941-179A-11
7	943	34.9	622	10	US-09-941-179A-3
8	933	34.5	502	9	US-10-157-031-92
9	928.5	34.4	631	10	US-09-941-179A-7
10	920.5	34.1	528	10	US-09-892-985-2
11	908	33.6	504	10	US-09-892-985-4
12	871.5	32.2	450	9	US-10-156-239-11
13	871.5	32.2	450	9	US-10-199-485-11
14	871.5	32.2	450	10	US-09-795-693-11
15	871	32.2	627	10	US-09-892-985-6
16	869	32.1	498	10	US-09-892-985-12
17	863.5	31.9	529	9	US-10-156-239-31
18	863.5	31.9	529	9	US-10-199-485-31
19	863.5	31.9	529	10	US-09-795-693-31

20	861	31.9	502	10	US-09-892-985-10	Sequence 10, Appl
21	842	31.2	457	9	US-10-157-031-28	Sequence 28, Appl
22	799	29.6	449	9	US-10-199-995-2	Sequence 2, Appl
23	621	23.0	520	9	US-10-012-542-144	Sequence 144, Appl
24	443.5	16.4	210	10	US-09-820-339A-2	Sequence 2, Appl
25	421	15.6	235	10	US-09-820-339A-6	Sequence 6, Appl
26	415	15.4	471	9	US-09-899-495-116	Sequence 116, Appl
27	413	15.3	230	10	US-09-820-339A-8	Sequence 8, Appl
28	395.5	14.6	447	10	US-09-955-524-9	Sequence 9, Appl
29	375	13.9	70	9	US-09-899-495-87	Sequence 87, Appl
30	373	13.8	441	10	US-09-732-680A-2	Sequence 2, Appl
31	294.5	10.9	132	9	US-09-899-495-86	Sequence 86, Appl
32	253.5	9.4	63	9	US-10-106-698-5644	Sequence 5644, Ap
33	232	8.6	485	10	US-09-808-483-12	Sequence 12, Appl
34	232	8.6	535	10	US-09-808-483-10	Sequence 39, Appl
35	210.5	7.8	440	9	US-09-510-662A-39	Sequence 39, Appl
36	210.5	7.8	440	10	US-09-778-320-39	Sequence 39, Appl
37	210.5	7.8	440	10	US-09-910-689-39	Sequence 39, Appl
38	210.5	7.8	440	12	US-10-010-742-39	Sequence 39, Appl
39	210.5	7.8	461	9	US-10-106-698-6308	Sequence 6308, Ap
40	208.5	7.7	417	9	US-10-075-846-2	Sequence 2, Appl
41	207.5	7.7	452	9	US-10-211-673-12	Sequence 12, Appl
42	202.5	7.5	357	9	US-09-899-495-118	Sequence 118, Appl
43	201.5	7.5	465	9	US-09-818-657-4	Sequence 4, Appl
44	197.5	7.3	431	9	US-10-075-846-4	Sequence 4, Appl
45	197.5	7.3	452	9	US-10-075-846-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1

US-09-954-936-2
; Sequence 2, Application US/09954936
; Publication No. US20030073161A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Clark A.
; APPLICANT: Gopalakrishnan, Murali
; APPLICANT: McKenna, David G.
; APPLICANT: Monteggia, Lisa M.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Sullivan, James P.
; APPLICANT: Touma, Edward
; APPLICANT: Abbott Laboratories
; TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR SUBUNIT, AND METHODS OF PRODUCTION AND USES THEREOF
; FILE REFERENCE: 6017.US.01
; CURRENT APPLICATION NUMBER: US/09/954,936
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 08/771,737
; PRIOR FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 502
; TYPE: PRT
; ORGANISM: homo sapien

Query Match 100.0%; Score 2703; DB 9; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.2e-251;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRCSPGVWLALAAASLLHVS	QGFQRLKYLKELVKNVNP	RPVANDSQPLTVFSL	60
Db	1	MRCSPGVWLALAAASLLHVS	QGFQRLKYLKELVKNVNP	RPVANDSQPLTVFSL	60
Qy	61	QIMDVDEKNQVLTNNIWLQSWTDHYLQWNVSEY	PGVKTVPRPGQIWKPDILL	YNSADE	120
Db	61	QIMDVDEKNQVLTNNIWLQSWTDHYLQWNVSEY	PGVKTVPRPGQIWKPDILL	YNSADE	120
Qy	121	RFDATFTNNVLSNGHCOYLP	PGIFKSSCCVIDVWF	PFDPVQHCCLKFGSWSYG	180
Db	121	RFDATFTNNVLSNGHCOYLP	PGIFKSSCCVIDVWF	PFDPVQHCCLKFGSWSYG	180

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Db 121 RFDAFHTNVLNNSGHCQYLPPIKSSCYIDVRWPPDPVQHCCKLKFGSWSYGGWSLDL 180
QY 181 QMQEADISGYIPNGEWDLVGIPKRSERFYECCKEYPDPVTFVTWRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPKRSERFYECCKEYPDPVTFVTWRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS 300
Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS 300
QY 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTIRVILLNWCWFLRMKPGEDKVRPACQHK 360
Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTIRVILLNWCWFLRMKPGEDKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPDPDGSVGCGRMACSPTDDEHL 420
Db 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPDPDGSVGCGRMACSPTDDEHL 420
QY 421 LHGGQPPGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFAACVVDRCLMAFSVFTI 480
Db 421 LHGGQPPGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFAACVVDRCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

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RESULT 2

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US-09-892-985-8
; Sequence 8, Application US/09892985
; Patent No. US20020111463A1
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/892,985
; FILING DATE: 27-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-98
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/466,589,
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9949B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-587-5360
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-892-985-8

Query Match          99.8%; Score 2698; DB 10; Length 502;
Best Local Similarity 99.8%; Pred. No. 3.7e-251;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAALASLLHVSLSQGFQKLYKELVKNYNPLRPVANDSQPLTVVFSLSLL 60
Db 1 MRCSPGGVWLAALASLLHVSLSQGFQKLYKELVKNYNPLRPVANDSQPLTVVFSLSLL 60
QY 61 QIMDVDEKNOVLTINIWLQMSWTDHYLQMNVSYPGVKTVRFPDQGIWKPDILLYNSADE 120
Db 61 QIMDVDEKNOVLTINIWLQMSWTDHYLQMNVSYPGVKTVRFPDQGIWKPDILLYNSADE 120
QY 121 RFDAFHTNVLNNSGHCQYLPPIKSSCYIDVRWPPDPVQHCCKLKFGSWSYGGWSLDL 180
Db 121 RFDAFHTNVLNNSGHCQYLPPIKSSCYIDVRWPPDPVQHCCKLKFGSWSYGGWSLDL 180
QY 181 QMQEADISGYIPNGEWDLVGIPKRSERFYECCKEYPDPVTFVTWRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPKRSERFYECCKEYPDPVTFVTWRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS 300
Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS 300
QY 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTIRVILLNWCWFLRMKPGEDKVRPACQHK 360
Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTIRVILLNWCWFLRMKPGEDKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPDPDGSVGCGRMACSPTDDEHL 420
Db 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPDPDGSVGCGRMACSPTDDEHL 420
QY 421 LHGGQPPGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFAACVVDRCLMAFSVFTI 480
Db 421 LHGGQPPGDPDLAKILEEVRYIANFRQCDESEAVCSEWKFAACVVDRCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

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RESULT 3

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US-09-303-232-6
; Sequence 6, Application US/09303232A
; Patent No. US20020006657A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Nucleic Acids which encode
; FILE OF INVENTION: Insect acetylcholine receptor subunits
; FILE REFERENCE: Le A 33 020-Foreign Countries
; CURRENT APPLICATION NUMBER: US/09/303,232A
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: DE 198 19 829.9
; EARLIER FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in ver. 2.1
; SEQ ID NO 6
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Heliothis virescens
US-09-303-232-6

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Query Match          46.4%; Score 1254.5; DB 10; Length 501;
Best Local Similarity 48.4%; Pred. No. 3.7e-112;
Matches 249; Conservative 75; Mismatches 139; Indels 51; Gaps 7;

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Qy 10 LALAAALLHVSLOGEFORGLYKELVKNYNPLERPVANDSOPLTVYFESLLOIMDVDEKN 69
Db 8 LALLA-LLPVSEQEPHEKRLNALNALTNTLIERVANESEPLEYRFGTLQOIIIDVDEKN 66
Qy 70 QVLTTNIWLOMSWTDHYLQWNVSEYPGVKTFRFPDGOIWKPDIIILYNSADERFDATFTN 129
Db 67 QLLITNIWLSLEWNYLNRWDSYGVKDLRIIPNKLWKPDVLMYNSADEGFGDTQTN 126
Qy 130 VLNVSSGHCQYLPPIGPKSSCYIDVRWFPDVOHQCKLKFGWSYGGWSLDLQWQE--AD 186
Db 127 VVVRSGSCLYVPPGIFKSTCKMDIAWFPDDQCHCDMKFGSWTYDGNQDLVLVDEAGGD 186
Qy 187 ISGYIPNGEWDLVIGPKRSERFECCKEYPDVTFTVMRRRTLYYGLNLLIIVGL 246
Db 187 LSDFITNGEYLLGMPGKNTIYACCEPYVDVFTIMIRRRRTLYYFFNLIVPCVLIS 246
Qy 247 LALLVFLPADSGEKISLIGITVLLSTFTFMLLVAEIMPATSDSVPLIAQYFASMTIIVGL 306
Db 247 MALLGFTLPDSEKLTGLVTILLSTVFNLVAETLPOVSDAIPLLGTVPNCIMFWAS 306
Qy 307 SVVTVTVIQLYHHDPDGGKMPKTRVILLNWCWFLMRKPGEDKVRPACQHKQRCSL 366
Db 307 SVLTVVLYNYHRTADIEHMPQWIKSVFLQWLPWILMRSPGKIKTRKTIMMTRREL 366
Qy 367 ASVEMSAVA-----PPP-----ASGNLLYIGFRGLDGVHCVPTPDSGVVC 407
Db 367 ELKERSKSLANLVLDIDDDFRHGPPPPNSTAGNL-----GPGC 407
Qy 408 G-----RWACSPTHDELLHGGOPPEGPDGLAKILEEVRVYIANRFRCODESAVCSW 460
Db 408 STFRDPRSFTVPSWEDV--GGUGSHREHLHLIRELOFITARMKKADEAEALISDW 465
Qy 461 KFAACVVDRLCLMAFSVFTIICITIGILMSAPNFV 494
Db 466 KFAAMVVDRCFLVFVFTLFTIIATVAVLLSAPHII 499

RESULT 4
US-09-303-232-4
; Sequence 4, Application US/09303232A
; Patent No. US20020006657A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Nucleic Acids which encode
; FILE REFERENCE: Le A 33 020-Foreign Countries
; CURRENT APPLICATION NUMBER: US/09/303,232A
; CURRENT FILING DATE: 1999-04-30
; EARLIER FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Heliothis virescens
US-09-303-232-4

Query Match 45.9%; Score 1242; DB 10; Length 496;
Best Local Similarity 45.8%; Pred. No. 5.8e-111;
Matches 239; Conservative 86; Mismatches 127; Indels 70; Gaps 6;

Qy 4 SPGWVWLAALASLLHVSLOGEFORGLYKELVKNYNPLERPVANDSOPLTVYFESLLOIM 63
Db 12 APAGLLLLCLLWPRGARGCYHEKRLHLHLHDHYNVLERPVNESDPLQSFGLTLMQII 71
Qy 64 DVDEKNOVLTNIWLOMSWTDHYLQWNVSEYPGVKTFRFPDGOIWKPDIIILYNSADERFD 123
Db 72 DVDEKNOVLTNIWLOMSWTDHYLQWNVSEYPGVKTFRFPDGOIWKPDIIILYNSADERFD 131
Qy 124 ATFTHTNLVNSGHCQYLPPIGPKSSCYIDVRWFPDVOHQCKLKFGWSYGGWSLDLQWQ 183
Db 132 STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPDDQRCCEMKFGSWTYDGYQLDLQLQ 191

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Qy 194 E---ADISGYIPNGEWDLVIGPKRSERFECCKEYPDVTFTVMRRRTLYYGLNLLIP 240
Db 192 DEGGDISSFYNTGEMWELIGVPGKNEIYYNCCPEYIDITFAVYIRKRLTYFFNLIYP 251
Qy 241 CVLISALALLVFLPADSGEKISLIGITVLLSTFTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 252 CVLIASALLGFTLPDPSGEKLSLGTVILLSTVFNVAETMPATSDAVPLGYFNCCI 311
Qy 301 MIIVGLSVVTVIQLYHHDPDGGKMPKTRVILLNWCWFLMRKPGEDKVRPACQHK 360
Db 312 MFVASSVVSITILYNYHRRHADTHEMSDWIRCVFLYWL PWVLRMSRPG----- 360
Qy 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPH---- 416
Db 361 -----SATTPPPAR-----VPPPPDLELRERSKSLANVLVD 392
Qy 417 -DEHLH-----CGQPPEG-----DPDLAKILEEVRVYIANRFRCODE 452
Db 393 IDDDFRHPQAQQOCCRYRGGEEAGLAAHSCFGVDYELSLILKEIRVITDQMRKODE 452
Qy 453 SEAVCSWKFAACVVDRLCLMAFSVFTIICITIGILMSAPNFV 494
Db 453 DADISRDKWKFAMVVDRLCLLIIFTLIIATLAVLLSAPHIM 494

RESULT 5
US-09-303-232-2
; Sequence 2, Application US/09303232A
; Patent No. US20020006657A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Nucleic Acids which encode
; FILE REFERENCE: Le A 33 020-Foreign Countries
; CURRENT APPLICATION NUMBER: US/09/303,232A
; CURRENT FILING DATE: 1999-04-30
; EARLIER FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-303-232-2

Query Match 42.7%; Score 1155.5; DB 10; Length 770;
Best Local Similarity 45.0%; Pred. No. 2.3e-102;
Matches 236; Conservative 82; Mismatches 116; Indels 91; Gaps 12;

Qy 8 VWLALASLLHVSLOGEFORGLYKELVKNYNPLERPVANDSOPLTVYFESLLOIMDVDE 67
Db 297 IYLNLSAK---VCLAGYHEKRLHLDLDPYNTLERPVNLNEDPLQLSFGTLTMOIIDVE 353
Qy 68 KNOVLTNIWLOMSWTDHYLQWNVSEYPGVKTFRFPDGOIWKPDIIILYNSADERFDATFH 127
Db 354 KNQLVTVNVLKLEWNDNMLRNWTSYGGVKDLRIIPHRIWKPDVLTNNSADEGFGDTYQ 413
Qy 128 TNVLVNSGHCQYLPPIGPKSSCYIDVRWFPDVOHQCKLKFGWSYGGWSLDLQWQE--- 184
Db 414 TNVVRNNGSCLYVPPGIFKSTCKIDITWFPDDQRCCEMKFGSWTYDGFQDLQLODETG 473
Qy 185 ADISGYIPNGEWDLVIGPKRSERFECCKEYPDVTFTVMRRRTLYYGLNLLIIPCVLI 244
Db 474 GDISSVYLVNGEWELLGVPGKNEIYYNCCPEYIDITFAIIRRTLYYFFNLIIPCVLI 533
Qy 245 SALALLVFLPADSGEKISLIGITVLLSTFTFMLLVAEIMPATSDSVPLIAQYFASMTIIV 304
Db 534 ASMALLGFTLPDPSGEKLSLGTVILLSTVFNVAETMPATSDAVPL----- 581
Qy 305 GLSVVTVIQLYHHDPDGGKMPKTRVILLNWCWFLMRKPGEDKVRP-ACQHKQR 363

```

Db 582 -----WIRIVFLCWLFWILRMSRPG-----RPLILEPPTTP 612
 Qy 364 CSLASVE-----MSAVAPPASNGNLY-----IGFRLDGVHCVp-TP-----401
 Db 613 CSDTSSERKHQILSDVELKERSKSLANVLDDDFRH-----NCRPMTFEGGLPHNPAF 668
 Qy 402 -----DSGVV-----CGRMASCPHDEHLHGGQPPEGDPDLAKILEVRVYIANRFR 449
 Db 669 YRTVYQGGDSIGPIGSTRMPDAVTH-----HTCIKSSTSEYELGLILKEIRITDQLR 723
 Qy 450 QDESEAVCSEWFAACVDRCLMAFSVFTIICITIGILMSAPNFV 494
 Db 724 DDECDIANDWKEFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768

RESULT 6

US-09-941-179A-11
 ; Sequence 11, Application US/09941179A
 ; Patent No. US20020146765A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bayer Aktiengesellschaft
 ; TITLE OF INVENTION: Acetylcholine receptor subunits
 ; FILE REFERENCE: Le A 34 821
 ; CURRENT APPLICATION NUMBER: US/09/941,179A
 ; CURRENT FILING DATE: 2001-08-27
 ; PRIOR APPLICATION NUMBER: DE 100 42 177.6
 ; PRIOR FILING DATE: 2000-08-28
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 11
 ; LENGTH: 622
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Modified alpha
 ; OTHER INFORMATION: 4 subunit of the chicken nicotinic acetylcholine
 ; OTHER INFORMATION: receptor
 US-09-941-179A-11

Query Match 35.5%; Score 959; DB 10; Length 622;
 Best Local Similarity 34.3%; Pred. No. 1.4e-83;
 Matches 209; Conservative 90; Mismatches 186; Indels 124; Gaps 9;
 Qy 4 SPGGWLAALASLL-----HVSLOGEFQKLYKELVKNYNPLERPVANDSOPLTIVYFSL 59
 Db 6 SKGNLLLLLCASIFPAFGHVETRAHAERLLKLFSGYNKWSRVPANISDVVLVRFGLSI 65
 Qy 60 LQIMDVDEKNOVLTTNIWLQMSWTDHYLQMNVSYPGVKTVRFPDGOIWKPDILLYNSAD 119
 Db 66 AQLIDVDEKNOQMTTNVWVQEWHDYKLRWDPQEVENVTSIRIPSELIRWPDIVLYNNAD 125
 Qy 120 ERDATHTNVLNNSGHCQYLPPIPKSSCYIDVRWPPFDVQHCKLKFSGWSYGGWSLD 179
 Db 126 GDFAVTHLTAKHLFYDGRIKWMPPIAYKSSCIDVTFPPFDQCKMKFGSWTYDKAKID 185
 Qy 180 L--QMEADISGYPNGEWDLVIGIPKRSERFECCKEPPDYDTFTVTMRRTLYYGLNL 237
 Db 186 LVSMHSHVDLSEFYSVEWDLVLEPAVRNEKFTYCCDEPYLDITFTNFIIRRLPLFYTNL 245
 Qy 238 LIPCVLISALALLVFLLPADSGEKISLIGITVLLSLTTFMLLVAIMPATDSVPLIAQYF 297
 Db 246 IIPCLLISCLTVLVFLYLPSECGEKILCISVLLSLTVFLLTITIIIPSTSLVPLIGEYL 305
 Qy 298 ASTMIIVGLSVVTVIVLYQHHHDPDGGKMPKTRVILLNCAWFLRMKRPG-----349
 Db 306 LFTMIFVTLIIITVFLNVHRSRPTHMPDWVRRVFLDIVPRLLFMKRPSTVDKNCCK 365
 Qy 350 -----EDKVRPACQHKOR 362
 Db 366 LIESMHLKLTNSPRLMSETDMEPNFTTSSPSQSNPSPTSSFCAHLEEPKMPCKSPG 425
 Qy 363 RCSLASVE---MSAVAPPPA-----SNGNLL-----YIGFRGLD 393

Db 426 QYSNLHPEPQVTCSSPKPSCHPLSDTQTTSISKGRSLSVQOQMYSPNKTBEGRSIRCRSRS 485
 Qy 394 GVHCVPPTDSGVVCGRMASCP-----HDEHLHL-----GQOPPEG-----429
 Db 486 IQCYILOEDSSQTNHSSASPAQRCHLNEEQPHKPHQCKCKRKGAAAGTPTQGSKSH 545
 Qy 430 -----DPLAKILEVRVYIANRFRQDSEAVCSEWFAACVDRCLMAFSVFT 479
 Db 546 SNKGEHLVMSLPALKLAVEGVHYIADHLRAEDADFSVKEDKYVMVIDRFLWMFIIVC 605
 Qy 480 IICITIGILM 488
 Db 606 LLGTVGLFL 614

RESULT 7

US-09-941-179A-3
 ; Sequence 3, Application US/09941179A
 ; Patent No. US20020146765A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bayer Aktiengesellschaft
 ; TITLE OF INVENTION: Acetylcholine receptor subunits
 ; FILE REFERENCE: Le A 34 821
 ; CURRENT APPLICATION NUMBER: US/09/941,179A
 ; CURRENT FILING DATE: 2001-08-27
 ; PRIOR APPLICATION NUMBER: DE 100 42 177.6
 ; PRIOR FILING DATE: 2000-08-28
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 622
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Modified alpha
 ; OTHER INFORMATION: 4 subunit of the chicken nicotinic acetylcholine
 ; OTHER INFORMATION: receptor
 US-09-941-179A-3

Query Match 34.9%; Score 943; DB 10; Length 622;
 Best Local Similarity 33.7%; Pred. No. 5e-82;
 Matches 205; Conservative 91; Mismatches 189; Indels 124; Gaps 9;
 Qy 4 SPGGWLAALASLL-----HVSLOGEFQKLYKELVKNYNPLERPVANDSOPLTIVYFSL 59
 Db 6 SKGNLLLLLCASIFPAFGHVETRAHAERLLKLFSGYNKWSRVPANISDVVLVRFGLSI 65
 Qy 60 LQIMDVDEKNOVLTTNIWLQMSWTDHYLQMNVSYPGVKTVRFPDGOIWKPDILLYNSAD 119
 Db 66 AQLIDVDEKNOQMTTNVWVQEWHDYKLRWDPQEVENVTSIRIPSELIRWPDIVLYNNAD 125
 Qy 120 ERDATHTNVLNNSGHCQYLPPIPKSSCYIDVRWPPFDVQHCKLKFSGWSYGGWSLD 179
 Db 126 GNFEVTLATKATLNTVGRVEMRPPAIYKSSCIDVVEYFPFQOQTCWKFSGSWTYDKAKID 185
 Qy 180 LQMEADIS--GYIPNGEWDLVIGIPKRSERFECCKEPPDYDTFTVTMRRTLYYGLNL 237
 Db 186 LVSMHSHVDLQDYWESGEWIIINAVGNVNSKKYECCTEYIPDITYFSIIRRLPLFYTNL 245
 Qy 238 LIPCVLISALALLVFLLPADSGEKISLIGITVLLSLTTFMLLVAIMPATDSVPLIAQYF 297
 Db 246 IIPCLLISCLTVLVFLYLPSECGEKILCISVLLSLTVFLLTITIIIPSTSLVPLIGEYL 305
 Qy 298 ASTMIIVGLSVVTVIVLYQHHHDPDGGKMPKTRVILLNCAWFLRMKRPG-----349
 Db 306 LFTMIFVTLIIITVFLNVHRSRPTHMPDWVRRVFLDIVPRLLFMKRPSTVDKNCCK 365
 Qy 350 -----EDKVRPACQHKOR 362
 Db 366 LIESMHLKLTNSPRLMSETDMEPNFTTSSPSQSNPSPTSSFCAHLEEPKMPCKSPG 425
 Qy 363 RCSLASVE---MSAVAPPPA-----SNGNLL-----YIGFRGLD 393

Db 426 QYSLHPEPPQVTCSSPKPSCHPLSDTQTTSISKRSLSVOQMYSPNKTBERGSIRCRSRS 485
 QY 394 GHVCTPTDPSGVCGRMACGPT-----HDEHLH-----GGQPPEG----- 429
 Db 486 IOCYLQEDSSQTNHSSASPASQORCHLNEBPQKHQCKCKRKGAAAGTPTQGSKSH 545
 QY 430 -----DPLAKILEEVRYIANRFRCODESEAVCESEKFAACVDRCLMAFVSFT 479
 Db 546 SNKGEHLVMSPALKLAVEGVHYIADHLRAEDADFSVKEDWKYVAMVIDRIFLWFIIVC 605
 QY 480 IICTIGILM 488
 Db 606 LLGTGVLFL 614

RESULT 8
 US-10-157-031-92
 ; Sequence 92, Application US/10157031
 ; Publication No. US20030108890A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baranova, A. V.
 ; APPLICANT: Yankovsky, N. K.
 ; APPLICANT: Kozlov, A. P.
 ; APPLICANT: Lobashev, A. V.
 ; APPLICANT: Krukovskaya, L. L.
 ; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
 ; FILE REFERENCE: 2760-103
 ; CURRENT APPLICATION NUMBER: US/10/157,031
 ; CURRENT FILING DATE: 2002-05-30
 ; NUMBER OF SEQ ID NOS: 415
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 92
 ; LENGTH: 502
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-157-031-92

Query Match 34.5%; Score 933; DB 9; Length 502;
 Best Local Similarity 37.7%; Pred. No. 3.4e-81;
 Matches 189; Conservative 92; Mismatches 166; Indels 54; Gaps 7;

QY 10 LALAASLLHVSLOGEFQKLYKELVKNYNPLRPVANDSOPLTIVYFSLSLQIMDVDEKN 69
 Db 16 LLLLSLLPVARASEAHLFERLFEDYNEIIRPVANVSDPVIHFVSMSQLVKVDEVN 75
 QY 70 QVLTNNIWLQMSWDHYLQNVSEYPCVKTVPDGOIKWPDILLNYSADERPDATHTN 129
 Db 76 QIMETNLWLQIMNDYKLNWPSGYGGAEMRPVPAQKIWKPDIVLYNNVAGDFQVITTK 135
 QY 130 VLNVSSGHQYLLPPGIFKSSCYIDVRWFPDVOHQCKLFGSWSYGGWSLDQM--QEADI 187
 Db 136 ALLKYTGVTWTPPAIFKSSCKIDVTYFPDYQNCITMKFGSWYDKAKIDLVLGSMNL 195
 QY 188 SGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRTLYYGLNLLIPCVLISAL 247
 Db 196 KDYESGEWAIKAPGYKHDIKYNCCEEIYPDITYSLYSRRLPLFTYINLIIPCLLISFL 255
 QY 248 ALLVLLPADSGEKISGITVLLSTFTMLVAEIMPATSDSVPPLIAQYFASWTMIIVGLS 307
 Db 256 TVLVFVLPDSCGEKVTLCISVLLSVFLVAVITETIPSTSLVPLIGEYLLFTMIFTLS 315
 QY 308 VVVTVLVQYHHDDPGGKMPKWTIRVILLNWCWFLRMKPEGDKVRPAQCHKQRRCSLA 367
 Db 316 IVITVFLNVHRTPTHTMPSVWVKTVFLMLLRVVMFMTRP-----T 357
 QY 368 SVMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDS-----GVVCGRMACSPTHDEHL-- 420
 Db 358 SNEGNAQKRPPLYGAE-----LSNLNCFSAESKGEKGYPCQDGMCGYCHRRIKI 409
 QY 421 -----LHGQPPEG-----DPLAKILEEVRYIANRFRCODESEAVCESEKFAA 464
 Db 410 SNFSANLTRSSSESVDVAVVSLSALSPEIKAEIQSVKYIAENMKQAQNEAKEIQDDWKYVA 469

QY 465 CVVDRLCLMAFVSFTIICTIG 485
 Db 470 MVIDRIFLW---VFTLVCLIG 487

RESULT 9
 US-09-941-179A-7
 ; Sequence 7, Application US/09941179A
 ; Patent No. US20020146765A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bayer Aktiengesellschaft
 ; TITLE OF INVENTION: Acetylcholine receptor subunits
 ; FILE REFERENCE: Le A 34 821
 ; CURRENT APPLICATION NUMBER: US/09/941,179A
 ; CURRENT FILING DATE: 2001-08-27
 ; PRIOR APPLICATION NUMBER: DE 100 42 177.6
 ; PRIOR FILING DATE: 2000-08-28
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 631
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Modified alpha
 ; OTHER INFORMATION: 4 subunit of the chicken nicotinic acetylcholine
 ; OTHER INFORMATION: receptor
 US-09-941-179A-7

Query Match 34.4%; Score 928.5; DB 10; Length 631;
 Best Local Similarity 33.3%; Pred. No. 1.3e-80;
 Matches 206; Conservative 90; Mismatches 189; Indels 133; Gaps 9;

QY 4 SPGCVMLALAASLL---HVSLOGEFQKLYKELVKNYNPLRPVANDSOPLTIVYFSLSL 59
 Db 6 SKGNLLLLLCASIPFAGCHVETRAHAERLUKLPFGSKYKNSRPRVANISDVVLVRFGLSI 65
 QY 60 LQIMDVDEKNQVLTNNIWLQMSWDHYLQNVSEYPCVKTVPDGOIKWPDILLNYSAD 119
 Db 66 AQLIDVDEKNQVLTNNIWLQMSWDHYLQNVSEYPCVKTVPDGOIKWPDILLNYSAD 125
 QY 120 ERDPATHTNNVNSSGHQYLLPPGIFKSSCYIDVRWFPDVOHQCKLFGSWSYGGWSLD 179
 Db 126 GDFAVTHLTKAHLFYDGRIKWMPPIAYKSSCIDVTFFPFPQONCKMFGSWYDKAKID 185
 QY 180 LMQEA-----DISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVWRR 228
 Db 186 LVSMHSHRGTVNVVELGVDQLDYWESGEWVIINAVGNYSKKYECCTETYPDITYSFIIR 245
 QY 229 RTLYYGLNLLIPCVLISALALLVLLPADSGEKISGITVLLSTFTMLVAEIMPATSD 288
 Db 246 LPUPYTNLIIPCLLISCLTVLVFYLSECEKVTLCISVLLSLTVFLLTEIIPSTLS 305
 QY 289 SVPLIAQYFASWTMIIVGLSVVVTVLVQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRP 348
 Db 306 VIPLIGEYLLFTMIIVGLSVVVTVLVQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRP 365
 QY 349 G-----EDKV 353
 Db 366 STVKDNCKLIESMHLKLTNSPRLMSETDMEPNFTTSSSPSPQSNPEPSTSSFCARLEP 425
 QY 354 RPACQHKQRRCSLASVE--MSAVAPPA-----SNGNLL----- 385
 Db 426 KPMCKSPSGQYMLHPEPPQVTCSSPKPSCHPLSDTQTTSISKRSLSVOQMYSPNKTBER 485
 QY 386 -YIGFRGLDGVHCVPTPDSGVVCGRMACSP-----HDEHLH-----GG 424
 Db 486 GSTRCRSRSIQCYLQEDSSQTNHSSASPASQORCHLNEBPQKHQCKCKRKGAAAG 545
 QY 425 QPPEG-----DPLAKILEEVRYIANRFRCODESEAVCESEKFAACVDRCL 470
 Db 546 TPTQGSKSHNKGEHLVMSPALKLAVEGVHYIADHLRAEDADFSVKEDWKYVAMVIDRI 605

QY	471	CLMAFSVFTI	CTIGILM	488
			:	:
		:	:	:
Db	606	FLWMFIIVCL	LGTVGFL	623

RESULT 10

```

US-09-892-985-2
; Sequence 2, Application US/098922985
; Patent No. US2002011463A1
; GENERAL INFORMATION:
;   INVENTOR: Ellis, Kathryn J.
;   ATTORNEY: Ellis, Steven B.
;   TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
;   RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME

```

```

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: Heller Ehrman White & McAuliffe
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA: . . .
APPLICATION NUMBER: US/09/892,985
FILING DATE: 27-Jun-2001

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/217,345
 FILING DATE: 21-DEC-98
 APPLICATION NUMBER: US 08/467,574
 FILING DATE: 05-JUN-95
 APPLICATION NUMBER: US 08/466,589,
 FILING DATE: 05-JUN-95
 APPLICATION NUMBER: US 08/028,031
 FILING DATE: 08-MAR-93

, ,
TIMING DATE: 08-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9949B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-450-8400
TELEFAX: 619-587-5360
TELEX: <Unknown>
:

```

? INFORMATION FOR SEQ ID NO: 2:
?
? SEQUENCE CHARACTERISTICS:
?     LENGTH: 528 amino acids
?     TYPE: amino acid
?     STRANDEDNESS: single
?     TOPOLOGY: unknown
?
? MOLECULE TYPE: protein
?
? SEQUENCE DESCRIPTION: SEQ ID NO: 2:
? US-09-892-985-2
?

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Query Match	34.1%;	Score 920.5;	DB 10;	Length 528;
Best Local Similarity	39.4%;	Pred. No. 5.8e-80;		
Matches 198; Conservative	77;	Mismatches 162;	Indels 65;	Gaps 10;

Qy	24	EFQRLKYLKVNPLERPVPANDSQPTVTYFSLQLQIMDVDEKNQVLTTNIWLQMSWT	83
Db	57	ETEDRLFCHLFRGNRWARPVPNTSDVIVRFGLSIAQLIDVDEKNQMTTNNVLKQWS	116
Qy	84	DHYLQWNVSEYPGVKTVRPPGQIWKPDILYNSADERPDATFHTNNVLVNSGHCQYLPP	143
Db	117	DYKLWNPADGNITSLRVPSEMIWPDILVYNKXGE-FVTHMTKAHLFTGTGVHWVPP	175
Qy	144	GIFKSSCYDIVRWPFDFVQHCKLXFGWSYSGWSLDLQMQE--ADISGYINGEWDLVGI	201
Db	176	AIYKSSGSDIVTFPFDDQNCMKFGSWTYQAKIDFLQMEGTVDLKDLYWSGSGWAIYNA	235


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; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/191,781
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-156-239-11

```

Query Match	32.2%	Score 871.5	DB 9	Length 450
Best Local Similarity	38.2%	Pred. No. 2.4e-75		
Matches 187	Conservative 81	Mismatches 164	Indels 57	Gaps 7
QY	12	LAASLLHVS	-----QGFQRLKLYELVKNVNP	LPVANDSQBLTVYFSLSLQIM 63
DB	8	LSGLGLLLSLFAECLGAEGSLAL	KFRDLPFANTYLSALRVPADTQ	PLNVTLEVTLSQII 67
QY	64	DVDEKQVLTNNIWLQMSWTBHYLQWNVSEY	PGVKTVRFPDGOIWKPDILLYNSAD	ERFD 123
DB	68	DMDERNQVLTLYLMIRQEWNTDAYLRWDPNAY	CGGLDAIRIPSSLVWRPDI	VLYNKADAQPP 127
QY	124	ATFTHTNLVNSGHCQYLP	PGGIFKSCYDIVRPPFDVQHC	KLKFGSWSYGGWSLDLQW 183
DB	128	GSASTNVVLRHDGAVRWDA	PAITRSSCKVDVAAPFPDAQ	HCGLTFGSWTHGGHQLDVRPR 187
QY	184	--EADISYVINGEWDLVG	IPGKSEFYECCKEYPDVTFTVM	TRRRTLYVGLNLLIPC 241
DB	188	GAASLADFVENRWRVGLMPARR	LVITYGCCSEYPDVTFTLLRRRAAY	VVCNLLLP 247
QY	242	VLISSALLVFLPADSGEKIS	LSGITVLLSLTTFMLIVAEIMPAT	SDSVPLIAQYFASTM 301
DB	248	VLISSLLAPLAPLADSGEKV	SLGVTVLLALTTFQLLLAESMP-	PAESVPLIGKYYMATM 306
QY	302	IIVGLSVVTVIVLYQYHHHPD	GGCKMPKTVRTVILLNCAWFLR	NKMPGDKVPRACQHKQ 361
DB	307	TWMTFTSTALTILIMNLHY	CGFSVRPVPAWARALLGHARL	CLVCRERGE---PCGQSRP 362
QY	362	RRCSLASVEMSAVAPPAS	NGNLLYIGFRGLDGVHCVPT	PTDSDGVVCGRMACSPTHDEHLL 421
DB	363	PELSPSPSGGAGPAG	-----PCHPRCLC-----	ROEALL 396
QY	422	HGGOPPEGDPDLAKILE	EVRYIANRFRCODESAVCS	EWKFAACVVDRLCLMAFSVTII 481
DB	397	H-----	HVATIANFESHRAAORCH	EDWKRIARVMDRFFLAIFFSMAIV 440

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QY      482 CTIGILMSA 490
      : : : |
Db      441 MSLVLVQA 449

RESULT 13
US-10-199-485-11
; Sequence 11, Application US/10199485
; Publication No. US20030077626A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: 20685, 579, 17114, 23821, 33894, and
; TITLE OF INVENTION: 32613, No. US20030077626A1el Human Transporters
; FILE REFERENCE: 35800/249468
; CURRENT APPLICATION NUMBER: US/10/199,485
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 09/795,693
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,906
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 450
; TYPE: PRT

```

```

; ORGANISM: Homo sapiens
US-10-199-485-11

Query Match      32.2%; Score 871.5; DB 9; Length 450;
Best Local Similarity 38.2%; Pred. No. 2.4e-75;
Matches 187; Conservative 81; Mismatches 164; Indels 57; Gaps 7;

QY 12 LAASLLHVSLL-----QGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIM 63
DB 8 LSLGILLLSLLPAECLGAEGRLALKLFRDLFANYTSALRPVADTQTLNVTLEVTLSQII 67

QY 64 DVDEKNOVLTTNIWLQMSWTDHYLQNVNSYEPGVKTVRFPDGOIKWPKDILLYNSADRF 123
DB 68 DMDEKNOVLTLWLIRQWTDAYLRWDPNAYGGLDAIRIPSSLVWRPDIIVLYNKADAQPP 127

QY 124 ATFTHTNVLNSSGHCQYLPPIKSSCYIDVRWFFPDVQHCKLKFGSWSYGGWLSLQIM 183
DB 128 GSASTNVVLRHGDGAVRWDAIPATIRSSCRVDVAAFPFDAQHCGLTFGSWTHGGHQLDVRPR 187

QY 184 --EADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVTRRRTLYYGLNLLIPC 241
DB 188 GAAASLADFVENVWRVGLMPARRVLTGCCSEPYDVTFTLLRRRAAYVNCNLLIPC 247

QY 242 VLISALALLVFLPADSGEKISIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAS 301
DB 248 VLISLAPLAFHLPADSGEKVSLGTVLLALTVPQLLAESMP-PAESVPLIGKYMATM 306

QY 302 IIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCAMFLRMKRGEDKVRPACQHK 361
DB 307 TMTVTFSTALTILIMNLHYCGSPVRPVPAMARALLGLHARGLCVRERGE----PCGQSRP 362

QY 362 RRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVVCGRMACSPHDEHLL 421
DB 363 PELSPSPQSPGAGPAG-----PCHEPRCLC-----RQALL 396

QY 422 HGGQPPGPDPAKILEEVRYIANFRCDSEAVCSWKFAACVDRCLCLMAFSVFTII 481
DB 397 H-----HVATIANFRSHRAAQCHEDKWLARVMDRFFLAIFFSMALV 440

QY 482 CTIGILMSA 490
DB 441 MSLVLLVQA 449

RESULT 14
US-09-795-693-11
; Sequence 11, Application US/09795693
; Patent No. US20020068710A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: 20685, 579, 17114, 23821, 33894, and
; FILE REFERENCE: 32613, No. US20020068710A1 Human Transporters
; CURRENT APPLICATION NUMBER: US/09795,693
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,906
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-693-11

Query Match      32.2%; Score 871.5; DB 10; Length 450;
Best Local Similarity 38.2%; Pred. No. 2.4e-75;
Matches 187; Conservative 81; Mismatches 164; Indels 57; Gaps 7;

QY 12 LAASLLHVSLL-----QGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIM 63
DB 8 LSLGILLLSLLPAECLGAEGRLALKLFRDLFANYTSALRPVADTQTLNVTLEVTLSQII 67

QY 64 DVDEKNOVLTTNIWLQMSWTDHYLQNVNSYEPGVKTVRFPDGOIKWPKDILLYNSADRF 123
DB 68 DMDEKNOVLTLWLIRQWTDAYLRWDPNAYGGLDAIRIPSSLVWRPDIIVLYNKADAQPP 127

QY 124 ATFTHTNVLNSSGHCQYLPPIKSSCYIDVRWFFPDVQHCKLKFGSWSYGGWLSLQIM 183
DB 128 GSASTNVVLRHGDGAVRWDAIPATIRSSCRVDVAAFPFDAQHCGLTFGSWTHGGHQLDVRPR 187

QY 184 --EADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVTRRRTLYYGLNLLIPC 241
DB 188 GAAASLADFVENVWRVGLMPARRVLTGCCSEPYDVTFTLLRRRAAYVNCNLLIPC 247

QY 242 VLISALALLVFLPADSGEKISIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAS 301
DB 248 VLISLAPLAFHLPADSGEKVSLGTVLLALTVPQLLAESMP-PAESVPLIGKYMATM 306

QY 302 IIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCAMFLRMKRGEDKVRPACQHK 361
DB 307 TMTVTFSTALTILIMNLHYCGSPVRPVPAMARALLGLHARGLCVRERGE----PCGQSRP 362

QY 362 RRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVVCGRMACSPHDEHLL 421
DB 363 PELSPSPQSPGAGPAG-----PCHEPRCLC-----RQALL 396

QY 422 HGGQPPGPDPAKILEEVRYIANFRCDSEAVCSWKFAACVDRCLCLMAFSVFTII 481
DB 397 H-----HVATIANFRSHRAAQCHEDKWLARVMDRFFLAIFFSMALV 440

QY 482 CTIGILMSA 490
DB 441 MSLVLLVQA 449

RESULT 15
US-09-892-985-6
; Sequence 6, Application US/09892985
; Patent No. US2002011463A1
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; Ellis, Steven B.
; Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/892,985
; FILING DATE: 27-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-98
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/466,589,
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9949B
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: 619-450-8400
TELEFAX: 619-587-5360
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 627 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-892-985-6

Query Match 32.2%; Score 871; DB 10; Length 627;
Best Local Similarity 33.1%; Pred. No. 4.3e-75;
Matches 202; Conservative 86; Mismatches 184; Indels 138; Gaps 11;

QY 10 LALAASLL---HVSLOGEQKLYKELAKNYPLEPVPANDSQPLTVYFSLSLLOIMDV 65
Db 17 LLGTGLLRASSHVETRAHAERLLKLFSGYNKSRPVANISDVLRFLGSLAQLIDV 76

QY 66 DEKNQVLTINILQMSWTDHYLQWNVSEYPCGKTVRPDGOIKPKDILLYNSADERFQAT 125
Db 77 DEKNQMTTNVVKQEHWDYKLRWDPADYENVTSIRIPSELIRPDIYALYNNADGDFAT 136

QY 126 FHTNVLVNSGHCQYLPFGIFKSSCYIDVRWFFDVQHCCLKFGWSYGGWSLDEL--QM 183
Db 137 HLTKAHLFDGRVORTFPATYKSSCIDVTFPPDQDQCTMKFGSWTYDKAKIDLNVNHS 196

QY 184 EADISGYPNGEWDLVCIPIGKRSEFYECCKEPPYDVTFTVMRRRTLYGLNLLIPCVL 243
Db 197 RVDQLDFWEGEMLIADAXGTYNTRKYECCEAIYPDIYAYAIRLPLFCTINILIPWL 256

QY 244 ISALALLVFLPADSGEKISIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASMTII 303
Db 257 ISCLTALVFLPSCGKILICISALLSLTGLLITTEIIPPTSLVPLIGEYLLFTMIF 316

QY 304 VGLSVVVTIVLQYHHHDPDGGKWKTRVILLNWCWFLMKPGEKVPACQHKQRR 363
Db 317 VTLISAIIVFVLNVHHSRTHMTPTWVRSVFLDIVPRLLLMKRP--SVVKDNC---R 369

QY 364 CSLASVEMSAVAP-----PPASNG----- 382
Db 370 RLIESMHKMASAPRFWPEPEGEPPATSGTQSLHPPSPFCVPLDVPAEPGSPCKSPDQL 429

QY 383 -----NLLYIGRG--LDG----- 394
Db 430 PPQKPLEAEKDSPPSPGCRPHGTOAPGLAKARSLVQHMSSPGEAVEGGVRCRSRI 489

QY 395 VHCVPPTDS---GVVCGRMACSPTHDEHLLHGGQP-----PEG----- 429
Db 490 QYCVPRDDAAPEADGQXAGLASENSHAELPPPDQSPCKCTCKEFPSSVPSAXVKTR 549

QY 430 -----DPDLAKILEVRYIANFRQDSEAVCSSEWKFACVDRCLCLMAFSVF 478
Db 550 STKAPPPHPLSPALSRAVEGVQYADHLKAEDTDFSVKEDWKYVANVIDRIFLWMFIIV 609

QY 479 TIICTIGILM 488
Db 610 CLLGTVGLFL 619

Search completed: June 20, 2003, 19:10:17
Job time : 55 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2003, 18:50:16 ; Search time 73 Seconds
(without alignments)

916.326 Million cell updates/sec

Title: US-09-954-936-2

Perfect score: 2703

Sequence: 1 MRCSPGVWIALAASLLHVS.....TIGILMSAPNFVAVSKDFA 502

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2703	100.0	502	19 AAW69216	V274T variant huma
2	2698	99.8	502	15 AAW44153	Human neuronal nic
3	2698	99.8	502	18 AAW09025	Neuronal nicotinic
4	2698	99.8	502	21 AAB24088	Human PRO2145 prot
5	2698	99.8	502	22 AAB82690	Nicotinic acetylch
6	2698	99.8	502	22 AAB50012	Wild-type human al
7	2692	99.6	502	22 AAB50015	Mutant human alpha
8	2688	99.4	502	22 AAB50016	Mutant human alpha
9	2682	99.2	502	22 AAB50017	Mutant human alpha
10	2429	89.9	502	18 AAW12368	Neuronal alpha-bun

11	1816.5	67.2	511	18 AAW12369	Neuronal alpha-bun
12	1474.5	54.6	470	22 AAB50014	Chimeric alpha7/5-
13	1360.5	50.3	448	22 AAB50018	Mature cell surfac
14	1254.5	46.4	501	21 AAY50816	H. virescens acety
15	1242	45.9	496	21 AAY50815	D. virescens acety
16	1155.5	42.7	770	21 AAY50814	D. melanogaster ac
17	1088	40.3	554	22 AAE12824	Caenorhabditis ele
18	975.5	36.1	631	23 AAO17243	Modified acetylcho
19	959	35.5	622	23 AAO17245	Modified acetylcho
20	959	35.5	622	23 ABB08885	Modified hen ACR s
21	954	35.3	311	22 ABB63683	Drosophila melanog
22	945	35.0	529	15 AAW44155	Human neuronal nic
23	945	35.0	529	16 AAR73966	Alpha 2 subunit of
24	945	35.0	529	18 AAW09021	Neuronal nicotinic
25	945	35.0	529	23 ABB61850	Prostate cancer-as
26	943	34.9	622	23 AAO17242	Modified acetylcho
27	943	34.9	622	23 ABB08883	Insect nicotinic A
28	935.5	34.6	576	22 ABB61954	Drosophila melanog
29	932	34.5	504	18 AAW09022	Neuronal nicotinic
30	928.5	34.4	631	23 AAO17244	Modified acetylcho
31	928.5	34.4	631	23 ABB08884	Modified hen ACR s
32	925.5	34.2	580	22 ABB62727	Drosophila melanog
33	917	33.9	502	22 AAB51021	JTF-38 nAChr alpha
34	916	33.9	627	18 AAW11824	Alpha4 subunit of
35	916	33.9	627	18 AAW09023	Neuronal nicotinic
36	913	33.8	495	11 AAR07143	Neuronal nicotinic
37	913	33.8	627	18 AAW11825	Alpha4 subunit of
38	887	32.8	727	15 AAW44152	Human neuronal nic
39	886	32.8	772	22 ABB59012	Drosophila melanog
40	884	32.7	498	18 AAW09027	Neuronal nicotinic
41	882	32.6	504	15 AAW44156	Human neuronal nic
42	881	32.6	498	15 AAW44154	Human neuronal nic
43	877	32.4	521	22 ABB70062	Drosophila melanog
44	871.5	32.2	450	22 AAG67161	Amino acid sequenc
45	867.5	32.1	433	22 AAU00402	Mature human alpha

ALIGNMENTS

RESULT 1
AAW69216
ID AAW69216 standard; Protein; 502 AA.
XX
AC AAW69216;
XX
DT 09-OCT-1998 (first entry)
XX
DE V274T variant human alpha7 nAChr protein.

Alpha7 nAChr; alpha7 nicotinic acetylcholine receptor subunit; cancer;
neurodegeneration; enzyme dysfunction; affective disorder; therapy;
immune dysfunction; diabetic neuropathy; Alzheimer's disease;
schizophrenia.

OS Homo sapiens.

XX

FN WO9828331-A2.

XX

PD 02-JUL-1998.

XX

PF 22-DEC-1997; 97WO-US23405.

XX

PR 20-DEC-1996; 96US-0771737.

XX

PA (ABBO) ABBOTT LAB.

XX

PI Briggs CA, Gopalakrishnan M, McKenna DG, Monteggia LM;

PI Roch J, Sullivan JP, Touma E;

XX

DR WPI; 1998-377593/32.

DR N-PSDB; AAV44687.

XX

PT Nucleic acid encoding variant of human alpha7 nicotinic
PT acetylcholine receptor sub-unit - used to identify modulators of
PT the receptor, potentially useful for treating neuro-degeneration,
XX cancer, affective disorders etc.
PS Claim 15; Fig 2; 44pp; English.
XX
CC This sequence is the V247T variant of human alpha7 nicotinic
CC acetylcholine receptor (nAChR) subunit of the invention. Cells containing
CC the DNA are used to express the protein and to identify modulators of
CC alpha7 nAChR activity or cytoprotective agents, e.g. antisense
CC compounds or antagonists that are potentially useful for treating
CC neurodegeneration, enzyme dysfunction, affective disorders and immune
CC dysfunction, such as cancer, post-herpetic neuralgia, diabetic
CC neuropathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru,
CC psychosis and schizophrenia. Probes based on the DNA are used to detect
CC the DNA in usual hybridisation or amplification tests, while monoclonal
CC antibodies are used to detect the protein for diagnosis (in vitro or by
CC in situ immuno-fluorescent assay). Compared with wild-type alpha7 nAChR,
CC the protein has about 100-fold greater sensitivity to cholinergic
CC receptor agonists (nicotine or acetylcholine) and response to these
CC agonists decays more slowly, but the wild-type inward rectification is
CC retained.
XX
SQ Sequence 502 AA;

Query Match 100.0%; Score 2703; DB 19; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.6e-260;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAASLLHVSLOGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
DQ |||||
Db 1 MRCSPGGVWLAASLLHVSLOGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
QY 61 QIMVDKQVLTNTIWLQMSWTDHYLQNVNVPYGVKTVRFPDQIWKPDILLYNSADE 120
DQ |||||
Db 61 QIMVDKQVLTNTIWLQMSWTDHYLQNVNVPYGVKTVRFPDQIWKPDILLYNSADE 120
QY 121 RDATEFTNVLNNSGHCQVLPFGIFKSSCYIDVRWFPDVOHCKLFGSWSYGGWSL 180
DQ |||||
Db 121 RDATEFTNVLNNSGHCQVLPFGIFKSSCYIDVRWFPDVOHCKLFGSWSYGGWSL 180
QY 181 QMQEADISGYPNGEWDLVGIPGRSRFYECKEPEYDPVTFVTMRRTLYGLNLLIP 240
DQ |||||
Db 181 QMQEADISGYPNGEWDLVGIPGRSRFYECKEPEYDPVTFVTMRRTLYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTFFMLLVAEIMPATSDSVPLIAQYF 300
DQ |||||
Db 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTFFMLLVAEIMPATSDSVPLIAQYF 300
QY 301 MIIVGLSVVTVTVLQYHHDDPGGKMPKTRVILLNWCWFLRMKPGEDKVRPACQHK 360
DQ |||||
Db 301 MIIVGLSVVTVTVLQYHHDDPGGKMPKTRVILLNWCWFLRMKPGEDKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRLDGVCHVCPVPDSCVCGRMACSPTHDEHL 420
DQ |||||
Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRLDGVCHVCPVPDSCVCGRMACSPTHDEHL 420
QY 421 LHGGQPEGDPDLAKILEEYRYIANFRFCQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
DQ |||||
Db 421 LHGGQPEGDPDLAKILEEYRYIANFRFCQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFEAVSKDFA 502
DQ |||||
Db 481 ICTIGILMSAPNFEAVSKDFA 502

RESULT 2

AAW44153

ID AAW44153 standard; Protein; 502 AA.

XX AAW44153;

XX

DT 14-MAY-1998 (first entry)
XX
DE Human neuronal nicotinic acetylcholine receptor alpha-7 subunit.
XX
KW Human; neuronal nicotinic acetylcholine receptor; alpha-7 subunit;
KW brain tissue; screening; NACHR; antibody.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Peptide 1..23
FT /label= signal
FT Domain 229..256
FT /label= TMD1
FT /note= "transmembrane domain"
FT Domain 262..284
FT /label= TMD2
FT /note= "transmembrane domain"
FT Domain 290..317
FT /label= TMD3
FT /note= "transmembrane domain"
FT Misc-difference 343
FT /note= "encoded by CTS"
FT Domain 462..487
FT /label= TMD4
FT /note= "transmembrane domain"
FT Domain 318..461
FT /label= cytoplasmic_loop
XX
PN W09420617-A2.
XX
PD 15-SEP-1994.
XX
PF 08-MAR-1994; 94WO-US02447.
XX
PR 08-MAR-1993; 93US-0028031.
XX
PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
PA (SIBI-) SIBIA NEUROSCIENCES INC.
XX
PI Elliott KJ, Ellis SB, Harpold MW;
XX
DR WPI; 1994-303024/37.
DR N-PSDB; AAV12197.
XX
XX Human neuronal nicotinic acetylcholine receptor subunits and DNA -
PT also transformed cells useful for screening cpds. which modulate
PT activity of the receptor
PT
PS Claim 7; Page 80-81; 99pp; English.
XX
CC The present sequence represents a human neuronal nicotinic acetylcholine
CC receptor (NACHR) subunit. The cells expressing the alpha and/or beta
CC NACHR subunits may be used in a method of screening compounds to
CC identify any which modulate the activity of human neuronal NACHR.
CC Subunit specific antibodies may be used to monitor the distribution
CC and expression density of various subunits in normal vs diseased brain
CC tissues. Testing of single receptor subunits or specific receptor
CC subunit combinations with a variety of potential agonists or antagonists
CC provides information with respect to the function and activity of the
CC individual subunits and should lead to the identification and design of
CC compounds that are capable of very specific interaction with one or
CC more receptor subtypes. The resulting drugs should exhibit fewer
CC unwanted side effects than drugs identified e.g. screening with cells
CC that express a variety of subtypes.
XX
SQ Sequence 502 AA;

Query Match 99.8%; Score 2698; DB 15; Length 502;
Best Local Similarity 99.8%; Pred. No. 5.2e-260;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      121 RFDAFTHTNVLVNSSGHCQVLPGLFKSSCYIDVRWPFDDVOHCKLKFSGWSYGSW 180
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Db      181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTVTMMRRRTLYYGLNLLIP 240
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QY      301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNCAWFLRMKRPGEKVRPACQHK 360
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Db      361 QRRCSLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY      421 LHGGQPEGPDLLAKILLEEVRYIANRFRQCDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
Db      421 LHGGQPEGPDLLAKILLEEVRYIANRFRQCDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
QY      481 ICTIGILMSAPNFVEAVSKDFA 502
Db      481 ICTIGILMSAPNFVEAVSKDFA 502

```

RESULT 3

AAW09025
ID AAW09025 standard; Protein; 502 AA.

XX AC AAW09025;

XX DT 09-APR-1997 (first entry)

XX DE Neuronal nicotinic acetylcholine receptor alpha-7 subunit.

XX KW Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
XX KW ligand-gated receptor.

XX OS Homo sapiens.

XX PN WO9641876-A1.

XX PD 27-DEC-1996.

XX PF 07-JUN-1996; 96WO-US09775.

XX PR 07-JUN-1995; 95US-0484722.

XX PA (SIBI-) SIBIA NEUROSCIENCES INC.

XX PI Elliott KJ, Harpold MW;

XX DR WPI; 1997-065463/06.

XX DR N-PSDB; AAT48239.

XX PT Nucleic acids encoding nicotinic acetylcholine receptor sub-units -

XX PT used in screening to determine the effect of drugs on the receptor

XX PS Disclosure; Page 73-74; 108pp; English.

XX CC The alpha-7 subunit (AAW09025) of the human neuronal nicotinic
XX CC acetylcholine receptor (nAChR) can be expressed in transformed

CC host cells carrying alpha-7 subunit DNA (see also AAT48239). Host
CC cells, esp. mammalian cells or amphibian oocytes, expressing the
CC recombinant alpha-7 subunit, opt. in combination with other
CC recombinant alpha and/or beta subunits (see also AAW09018-24,
CC AAW09026-27), can be used to examine the function of human AChR and
CC to identify cpds. that modulate its activity.

SQ Sequence 502 AA;

Query Match 99.8%; Score 2698; DB 18; Length 502;

Best Local Similarity 99.8%; Pred. No. 5.2e-260;

Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQMNVSYPGVKTVRPPDQGIWKPDILLYNSADE 120
QY      121 RFDAFTHTNVLVNSSGHCQVLPGLFKSSCYIDVRWPFDDVOHCKLKFSGWSYGSW 180
Db      121 RFDAFTHTNVLVNSSGHCQVLPGLFKSSCYIDVRWPFDDVOHCKLKFSGWSYGSW 180
QY      181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTVTMMRRRTLYYGLNLLIP 240
Db      181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTVTMMRRRTLYYGLNLLIP 240
QY      241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db      241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
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Db      301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNCAWFLRMKRPGEKVRPACQHK 360
QY      361 QRRCSLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db      361 QRRCSLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
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Db      421 LHGGQPEGPDLLAKILLEEVRYIANRFRQCDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
QY      481 ICTIGILMSAPNFVEAVSKDFA 502
Db      481 ICTIGILMSAPNFVEAVSKDFA 502

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RESULT 4

AAW09025
ID AAW09025 standard; Protein; 502 AA.

XX AC AAW09025;

XX DT 29-JAN-2001 (first entry)

XX DE Human PRO2145 protein sequence SEQ ID NO:77.

XX KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
XX KW proliferation; tumorigenesis; identification; cancer; cytostatic;
XX KW neurotropic; neuroprotective; antiinflammatory; immunosuppressive;
XX KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
XX KW neuronal disorder; glioma disorder; astrocytoma disorder; angiogenic;
XX KW epithelial disorder; glandular disorder; macrophage disorder;
XX KW inflammatory disorder; immunologic disorder.

XX OS Homo sapiens.

XX PN WO2000053755-A2.

PD 14-SEP-2000.
XX PF 06-JAN-2000; 2000WO-US00376.
XX PR 08-MAR-1999; 99WO-US05028.
XX PR 02-JUN-1999; 99WO-US12252.
XX PR 23-JUN-1999; 99US-0141037.
XX PR 07-JUL-1999; 99US-0143048.
XX PR 26-JUL-1999; 99US-0145698.
XX PR 30-NOV-1999; 99WO-US28313.
XX PR 20-DEC-1999; 99WO-US30911.
XX PR 05-JAN-2000; 2000WO-US00219.
XX (GETH) GENENTECH INC.
XX AShtenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
XX Watanabe CK, Wood WI;
XX WPI; 2000-572270/53.
XX N-PSDB; AAC58395.
XX DR
XX PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
XX treatment, diagnosis and prevention of cancer -
XX PS Claim 61; Fig 58; 286pp; English.
XX CC The present invention describes an isolated antibody that binds to
XX one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,
XX PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,
XX PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,
XX PRO1187, PRO1281, PRO239, PRO834, PRO1317, PRO1710, PRO2094,
XX PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell
XX growth. The PRO polypeptides and nucleotides are useful in the
XX treatment, diagnosis and prevention of cancer. The antibodies and other
XX anti-tumour compounds may be used to treat various conditions, including
XX those characterised by overexpression and/or activation of the amplified
XX PRO genes. Exemplary conditions or disorders to be treated with such
XX antibodies and other compounds include benign or malignant tumours
XX (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,
XX colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic
XX carcinomas, sarcomas, glioblastomas, and various head and neck tumours),
XX leukaemias and lymphoid malignancies, other disorders such as neuronal,
XX glial, astrocytic, hypothalamic and other glandular, macrophagal,
XX epithelial, stromal and blastocoeolic disorders, and inflammatory,
XX angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR
XX primers and hybridisation probes used in the isolation of the human PRO
XX sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human
XX PRO polynucleotide and protein sequences given in the exemplification of
XX the present invention.
XX SQ Sequence 502 AA;
Query Match 99.8%; Score 2698; DB 21; Length 502;
Best Local Similarity 99.8%; Pred. No. 5.2e-260;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRCSPGGVWLAALASLLHVSLSQGFQKLYKELVKNVKNPLRPVANDSQPLTVFSL 60
DB 1 MRCSPGGVWLAALASLLHVSLSQGFQKLYKELVKNVKNPLRPVANDSQPLTVFSL 60
QY 61 QIMDVDEKNQVLTINWLSWTDHYLQWNVSEYGVKTVFPDGOIWKPDILLYNSADE 120
DB 61 QIMDVDEKNQVLTINWLSWTDHYLQWNVSEYGVKTVFPDGOIWKPDILLYNSADE 120
QY 121 RFDATEFTNVLVNSGHCQYLPPIGIFKSSCYIDVRWPFQVQCKLKEGWSYGSWLDL 180
DB 121 RFDATEFTNVLVNSGHCQYLPPIGIFKSSCYIDVRWPFQVQCKLKEGWSYGSWLDL 180
QY 181 QMQEADISGYIPNGEWDLVIGPKRSEFYECCKEPYDPVFTVTMRRTLYYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVIGPKRSEFYECCKEPYDPVFTVTMRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTTFVLMVAIMPATSDSVPLIAQYFAST 300

DB 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTTFVLMVAIMPATSDSVPLIAQYFAST 300.
QY 301 MIIVGLSVVTVTVIQLYHHDDPGGKMPKTRVILLNWCANFLMRKRGEDKVRPACQHK 360
DB 301 MIIVGLSVVTVTVIQLYHHDDPGGKMPKTRVILLNWCANFLMRKRGEDKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGMACSPTHDEHL 420
DB 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGMACSPTHDEHL 420
QY 421 LHGGQPEGDDDLAKILEEVRYIANFRQCDESAVCESEKFAACVVDRLCLIMAFSVFTI 480
DB 421 LHGGQPEGDDDLAKILEEVRYIANFRQCDESAVCESEKFAACVVDRLCLIMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502
RESULT 5
AAB82690
ID AAB82690 standard; Protein; 502 AA.
XX AC AAB82690;
XX DT 15-OCT-2001 (first entry)
XX DE Nicotinic acetylcholine receptor alpha7.
XX KW Nicotinic acetylcholine receptor; nAChR; human;
XX KW acetylcholine binding protein; AChBP; mollusc;
XX KW ligand-binding protein; ligand-gated ion channel; crystal;
XX KW drug design; protein co-ordinate data; schizophrenia;
XX KW Alzheimer's disease; nicotine addiction; Tourette's syndrome;
XX KW therapy; neurotropic; neuroprotective.
XX OS Homo sapiens.
XX FH Key
XX FT Region 108..115
XX FT /note= "conserved ligand-binding region, residues
XX FT Trp108 and Tyr115 are essential"
XX FT Region 171..173
XX FT /note= "conserved ligand-binding region, residues
XX FT Trp171 and Tyr173 are essential"
XX FT Region 210..217
XX FT /note= "conserved ligand-binding region, residues
XX FT Tyr210, Cys212, Cys213 and Tyr217 are
XX FT essential"
XX PN WO200158951-A2.
XX XX
XX PD 16-AUG-2001.
XX XX
XX PF 09-FEB-2001; 2001WO-EP01457.
XX XX
XX PR 10-FEB-2000; 2000EP-0200443.
XX PR 31-OCT-2000; 2000EP-0203810.
XX XX
XX PA (TEWE-) STICHTING TECH WETENSCHAPPEN.
XX XX
XX PI Smit AB, Sixma TK;
XX XX
XX DR WPI; 2001-497071/54.
XX XX
XX PT Water-soluble ligand-binding proteins derived from molluscs and analogues
XX PT of ligand-gated ion channels, useful in drug screening assay, where the
XX PT drugs identified can be used in the treatment of Alzheimer's disease or
XX PT schizophrenia -
XX PS Disclosure; Page 252-254; 260pp; English.

CC The present sequence is that of the alpha subunit of human
 CC nicotinic acetylcholine receptor (nAChR). The sequence includes
 CC regions that are conserved throughout the various nAChR alpha
 CC subunits and which are essential for ligand binding. The invention
 CC relates to water-soluble ligand-binding proteins derived from
 CC molluscs, especially acetylcholine-binding proteins (AChBPs) and
 CC analogues of ligand-gated ion channels, their crystals, and their
 CC use for screening ligands of ligand-gated ion channels. The
 CC water-soluble ligand-binding proteins are capable of forming
 CC multimers and are amenable to crystallization. The crystal
 CC structure of AChBP is provided, and can be used to generate 3D
 CC models of the extracellular ligand-binding domain of ligand-gated
 CC ion channels and thus for screening of drugs that act on these
 CC ion channels. Chimeric proteins are provided that are capable of
 CC binding a ligand of a ligand-gated receptor, and comprise at
 CC least the amino acids of the AChBP determining solubility of the
 CC AChBP, in the same positions as in the AChBP, and also comprising
 CC amino acids determining binding to the ligand. In the chimeric
 CC proteins, at least the essential amino acids of at least 1 of the
 CC conserved regions of an nAChR have been substituted for the
 CC corresponding amino acids, and preferably entire stretches have
 CC been substituted. New drugs can be developed that selectively
 CC intervene in neuronal signalling pathways, especially where the
 CC ligand-gated ion channel is the nAChR, and the related disorder is
 CC Tourette's syndrome, Alzheimer's disease, addiction to nicotine
 CC or schizophrenia.
 CC
 XX
 SQ Sequence 502 AA;

Query Match 99.8%; Score 2698; DB 22; Length 502;
 Best Local Similarity 99.8%; Pred. No. 5.2e-260;
 Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLALAAASLLHVSLSQGFQKLYKELVKNYNPLRPVANDSQPLTVVFSLSLL 60
 DB 1 MRCSPGGVWLALAAASLLHVSLSQGFQKLYKELVKNYNPLRPVANDSQPLTVVFSLSLL 60
 QY 61 QIMDVDEKNOVLTTNIWLQMSWTDHYLQMNVSYPGVKTVRFPDQGIWKPDILLYNSADE 120
 DB 61 QIMDVDEKNOVLTTNIWLQMSWTDHYLQMNVSYPGVKTVRFPDQGIWKPDILLYNSADE 120
 QY 121 RFDATEFTNVLNVSSGHCQVLPFGIFKSSCYIDVRWPFDFVQHCKLKFSGWSYGGWSL 180
 DB 121 RFDATEFTNVLNVSSGHCQVLPFGIFKSSCYIDVRWPFDFVQHCKLKFSGWSYGGWSL 180
 QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIP 240
 DB 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIP 240
 QY 241 CVLISALALLVFLLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 DB 241 CVLISALALLVFLLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVTVIVLQYHHHDPDGGKMPKTRVILLNWCWFLRMKRPGEKVRPAQCHK 360
 DB 301 MIIVGLSVVTVIVLQYHHHDPDGGKMPKTRVILLNWCWFLRMKRPGEKVRPAQCHK 360
 QY 361 QRCCLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 DB 361 QRCCLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 QY 421 LHGGQPPGDPDLAKILEEVRYIANRFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 DB 421 LHGGQPPGDPDLAKILEEVRYIANRFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFEAVSKDFA 502
 DB 481 ICTIGILMSAPNFEAVSKDFA 502

RESULT 6
 AAB50012
 ID AAB50012 standard; Protein; 502 AA.

XX AAB50012;
 AC 14-MAR-2001 (first entry)
 DT
 XX Wild-type human alpha7 ligand gated ion channel.
 DE
 XX Human; alpha7 nicotinic acetylcholine gated ion channel;
 KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance.
 KW
 OS Homo sapiens.
 OS
 PN WO2000073431-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 25-MAY-2000; 2000WO-US11862.
 XX
 PR 27-MAY-1999; 99US-0136174.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Groppi VE, Wolfe ML, Berkenpas MB;
 XX
 DR WPI; 2001-061524/07.
 DR
 DR N-ESDB; AAC90380.
 XX
 PT Special cell culture medium for treating cells and for inducing
 PT mammalian cell lines to conduct calcium ions, comprising specified
 PT concentrations of ions of sodium, calcium and potassium at specified pH
 PT
 PS Disclosure; Pages 61-63; 77pp; English.
 XX
 CC The present sequence is wild-type human alpha7 nicotinic acetylcholine
 CC gated ion channel. The human alpha7 ion channel was used in the
 CC construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand
 CC gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric
 CC ion channel can be expressed by recombinant cells in the present
 CC invention, resulting in preferential calcium ion conductance by the
 CC cells.
 CC
 SQ Sequence 502 AA;

Query Match 99.8%; Score 2698; DB 22; Length 502;
 Best Local Similarity 99.8%; Pred. No. 5.2e-260;
 Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLALAAASLLHVSLSQGFQKLYKELVKNYNPLRPVANDSQPLTVVFSLSLL 60
 DB 1 MRCSPGGVWLALAAASLLHVSLSQGFQKLYKELVKNYNPLRPVANDSQPLTVVFSLSLL 60
 QY 61 QIMDVDEKNOVLTTNIWLQMSWTDHYLQMNVSYPGVKTVRFPDQGIWKPDILLYNSADE 120
 DB 61 QIMDVDEKNOVLTTNIWLQMSWTDHYLQMNVSYPGVKTVRFPDQGIWKPDILLYNSADE 120
 QY 121 RFDATEFTNVLNVSSGHCQVLPFGIFKSSCYIDVRWPFDFVQHCKLKFSGWSYGGWSL 180
 DB 121 RFDATEFTNVLNVSSGHCQVLPFGIFKSSCYIDVRWPFDFVQHCKLKFSGWSYGGWSL 180
 QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIP 240
 DB 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIP 240
 QY 241 CVLISALALLVFLLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 DB 241 CVLISALALLVFLLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVTVIVLQYHHHDPDGGKMPKTRVILLNWCWFLRMKRPGEKVRPAQCHK 360
 DB 301 MIIVGLSVVTVIVLQYHHHDPDGGKMPKTRVILLNWCWFLRMKRPGEKVRPAQCHK 360
 QY 361 QRCCLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420

XX The present sequence is a mutant human alpha7 nicotinic acetylcholine
CC gated ion channel. The human alpha7 ion channel was used in the
CC construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand
CC gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric
CC ion channel can be expressed by recombinant cells in the present
CC invention, resulting in preferential calcium ion conductance by the
CC cells.

XX SQ Sequence 502 AA;

Query Match 99.4%; Score 2688; DB 22; Length 502;
Best Local Similarity 99.6%; Pred. No. 5.1e-259;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MRCSPGGVWLALAAASLLHVSLSQGEFQRLKYLKELVKNYNPLERPVPANDSQPLTVVFSLSLL 60
Db 1 MRCSPGGVWLALAAASLLHVSLSQGEFQRLKYLKELVKNYNPLERPVPANDSQPLTVVFSLSLL 60

Qy 61 QIMDVDEKQVLTNTNIWLQMSWTDHYLQMNVSYPGVKTVRFPDQGIWKPDILLYNSADE 120
Db 61 QIMDVDEKQVLTNTNIWLQMSWTDHYLQMNVSYPGVKTVRFPDQGIWKPDILLYNSADE 120

Qy 121 RFDATFHTNVLNNSGHCQYLPGIFKSSCYIDVRWEPFDVQHCCLKFGSWSGWSL 180
Db 121 RFDATFHTNVLNNSGHCQYLPGIFKSSCYIDVRWEPFDVQHCCLKFGSWSGWSL 180

Qy 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTMRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTMRRTLYYGLNLLIP 240

Qy 241 CVLISALALVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 SVLISALALVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300

Qy 301 MIIVGLSVVTVTVLQYHHHDPGGMKPKWTRVILLNWCWFLRMKRPGEKVRPACQHK 360
Db 301 MIIVGLSVVTVTVLQYHHHDPGGMKPKWTRVILLNWCWFLRMKRPGEKVRPACQHK 360

Qy 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420

Qy 421 LHGGQPPEGDPDLAKILEEVRYIANFRFCQDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANFRFCQDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480

RESULT 9
AAB50017
ID AAB50017 standard; Protein; 502 AA.
XX AC AAB50017;
XX DT 14-MAR-2001 (first entry)
XX DE Mutant human alpha7 ligand gated ion channel #3.
XX KW Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;
XX OS 5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutein.
XX OS Homo sapiens.
XX OS Synthetic.

XX FH Key Location/Qualifiers
FT Misc-difference 230
FT FT /note= "Wild-type Thr substituted by Pro"
FT FT Misc-difference 241
FT FT /note= "Wild-type Cys substituted by Ser"

XX PN WO200073431-A2.
XX PD 07-DEC-2000.
XX PF 25-MAY-2000; 2000WO-US11862.
XX PR 27-MAY-1999; 99US-0136174.
XX PA (PHAA) PHARMACIA & UPJOHN CO.
XX PI Groppi VE, Wolfe ML, Berkenpas MB;
XX WPI; 2001-061524/07.
XX N-PSDB; AAC90387.
XX Special cell culture medium for treating cells and for inducing
XX mammalian cell lines to conduct calcium ions, comprising specified
XX concentrations of ions of sodium, calcium and potassium at specified pH
XX Claim 104; Pages 75-77; 77pp; English.
XX The present sequence is a mutant human alpha7 nicotinic acetylcholine
XX gated ion channel. The human alpha7 ion channel was used in the
XX construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand
XX gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric
XX ion channel can be expressed by recombinant cells in the present
XX invention, resulting in preferential calcium ion conductance by the
XX cells.

XX SQ Sequence 502 AA;

Query Match 99.2%; Score 2682; DB 22; Length 502;
Best Local Similarity 99.4%; Pred. No. 2e-258;
Matches 499; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MRCSPGGVWLALAAASLLHVSLSQGEFQRLKYLKELVKNYNPLERPVPANDSQPLTVVFSLSLL 60
Db 1 MRCSPGGVWLALAAASLLHVSLSQGEFQRLKYLKELVKNYNPLERPVPANDSQPLTVVFSLSLL 60

Qy 61 QIMDVDEKQVLTNTNIWLQMSWTDHYLQMNVSYPGVKTVRFPDQGIWKPDILLYNSADE 120
Db 61 QIMDVDEKQVLTNTNIWLQMSWTDHYLQMNVSYPGVKTVRFPDQGIWKPDILLYNSADE 120

Qy 121 RFDATFHTNVLNNSGHCQYLPGIFKSSCYIDVRWEPFDVQHCCLKFGSWSGWSL 180
Db 121 RFDATFHTNVLNNSGHCQYLPGIFKSSCYIDVRWEPFDVQHCCLKFGSWSGWSL 180

Qy 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTMRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTMRRTLYYGLNLLIP 240

Qy 241 CVLISALALVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 SVLISALALVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300

Qy 301 MIIVGLSVVTVTVLQYHHHDPGGMKPKWTRVILLNWCWFLRMKRPGEKVRPACQHK 360
Db 301 MIIVGLSVVTVTVLQYHHHDPGGMKPKWTRVILLNWCWFLRMKRPGEKVRPACQHK 360

Qy 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420

Qy 421 LHGGQPPEGDPDLAKILEEVRYIANFRFCQDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANFRFCQDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480

Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

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RESULT 10
AAW12368
ID AAW12368 standard; Protein; 502 AA.
XX
AC AAW12368;
XX
DT 17-JUN-1997 (first entry)
XX
DE Neuronal alpha-bungarotoxin binding protein alpha1 subunit.
XX
KW Neuronal alpha-bungarotoxin binding protein alpha 1; cholinergic;
KW ligand binding; ion channel.
XX
OS Gallus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..22
FT Protein /label= Sig_peptide
FT /label= Mat_protein
XX
PN US5599709-A.
XX
PD 04-FEB-1997.
XX
PF 28-SEP-1989; 89US-0413947.
XX
PR 28-SEP-1989; 89US-0413947.
XX
PA (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
PI Lindstrom JM, Schoepfer RD;
XX
DR WPI; 1997-118297/11.
DR N-PSDB; AAT59196.
XX
PT New isolated neuronal alpha-bungarotoxin-binding protein DNA - used
PT to screen cholinergic agents and other drugs which may affect ligand
PT binding, ion channel or other activities of the protein.
XX
PS Example; Fig 2A-B; 18pp; English.
XX
CC The alpha1 subunit (AAW12368) and alpha2 subunit (AAW12369) amino acid
CC sequences of chick neuronal alpha-bungarotoxin binding protein
CC obtd. from an 18-day chick embryo cDNA library. ABBP subunits can
CC be produced in recombinant host cells, pref. a bacterium, and used
CC in the screening of cholinergic agents and other drugs that may
CC affect the ligand binding, ion channel or other activity of intact
CC ABBP subtypes. The ABBP alpha1 and alpha2 subunits can also be
CC used to produce subunit peptides for use as immunogens for
CC preparing antibodies to permit affinity purification of subtypes
CC and their histological location.
XX
SQ Sequence 502 AA;

Query Watch 89.9%; Score 2429; DB 18; Length 502;
Best Local Similarity 90.7%; Pred. No. 3.5e-233;
Matches 449; Conservative 18; Mismatches 28; Indels 0; Gaps 0;

QY 8 VMLAASLHVSLOGEFORLYKELVKNYNPLRPVANDSQPLTVFSLQIMDYDE 67
DB 8 LWLLAAAGLVRESLQGEFORLYKELVKNYNPLRPVANDSQPLTVFSLQIMDYDE 67
QY 68 KNOVLTNIWLQSWTDHYLQWNVSEYPGVKTVPFPGQIWKPDILLVNSADERFDATFH 127
DB 68 KNOVLTNIWLQWTDHYLQWNVSEYPGVKNVFPDGLIWKPDILLVNSADERFDATFH 127
QY 128 TNVLVNSSGHGQYLPPGIFKSSCYIDVRWPFDFVQHCKLKFSGWSYGGWSDLQMOEADI 187
DB 128 TNVLVNSSGHGQYLPPGIFKSSCYIDVRWPFDFVQKCNLKFSGWSYGGWSDLQMOEADI 187

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188 SGYIPNGEWDLVGIPIGRSERFYECCKEYPDVTFTVTRRTLYYGNLLIPCVLISAL 247
188 SGYISNGEWDLVGIPIGRKTESFYECCKEYPDITFTVTRRTLYYGNLLIPCVLISAL 247
248 ALLVFLLPADSGEKISLIGITVLLSLTTFMLVAEIMPATSDVPLIAQYFASTMIIVGLS 307
248 ALLVFLLPADSGEKISLIGITVLLSLTTFMLVAEIMPATSDVPLIAQYFASTMIIVGLS 307
308 VVTVTVVLQYHHDPDGGKMPKTRVILLNWCAMFLRMKRPGEKVRPACQKQRCSLA 367
308 VVTVTVVLQYHHDPDGGKMPKTRVILLNWCAMFLRMKRPGEKVRPACQKQRCSLS 367
368 SVENSAPPPASNGNLLYIGFRLDGVHCVPDPDSGVVCGRMACSPHDEHLLHGGOPP 427
368 SMEMTVSGQOCNGNMLYIGFRLDGVHCPTPTTDSGVICGRMTCSPTEENLLSHGHP 427
428 EGGDPLAKILLEEVRYIANFRCODESEAVCSWEKFAACVVDRLCLMAFSVFTIICIGIL 487
428 EGGDPLAKILLEEVRYIANFRDQDEEAICNEWKFAASVVDRLCLMAFSVFTIICIGIL 487
488 MSAPNFVEAVSKDFA 502
488 MSAPNFVEAVSKDFA 502

RESULT 11
AAW12369
ID AAW12369 standard; Protein; 511 AA.
XX
AC AAW12369;
XX
DT 17-JUN-1997 (first entry)
XX
DE Neuronal alpha-bungarotoxin binding protein alpha2 subunit.
XX
KW Neuronal alpha-bungarotoxin binding protein alpha 2; cholinergic;
KW ligand binding; ion channel.
XX
OS Gallus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT Protein /label= Sig_peptide
FT /label= Mat_protein
XX
PN US5599709-A.
XX
PD 04-FEB-1997.
XX
PF 28-SEP-1989; 89US-0413947.
XX
PR 28-SEP-1989; 89US-0413947.
XX
PA (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
PI Lindstrom JM, Schoepfer RD;
XX
DR WPI; 1997-118297/11.
DR N-PSDB; AAT59197.
XX
PT New isolated neuronal alpha-bungarotoxin-binding protein DNA - used
PT to screen cholinergic agents and other drugs which may affect ligand
PT binding, ion channel or other activities of the protein.
XX
PS Example; Fig 3A-B; 18pp; English.
XX
CC The alpha1 subunit (AAW12368) and alpha2 subunit (AAW12369) amino acid
CC sequences of chick neuronal alpha-bungarotoxin binding protein
CC (ABBP) were deduced from newly isolated DNA molecules (AAT59196-97)
CC obtd. from an 18-day chick embryo cDNA library. ABBP subunits can
CC be produced in recombinant host cells, pref. a bacterium, and used
CC in the screening of cholinergic agents and other drugs that may
CC affect the ligand binding, ion channel or other activity of intact
CC ABBP subtypes. The ABBP alpha1 and alpha2 subunits can also be
CC used to produce subunit peptides for use as immunogens for
CC preparing antibodies to permit affinity purification of subtypes
CC and their histological location.
XX
SQ Sequence 511 AA;

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CC affect the ligand binding, ion channel or other activity of intact
 CC ABAP subtypes. The ABAP alpha1 and alpha2 subunits can also be
 CC used to produce subunit peptides for use as immunogens for
 CC preparing antibodies to permit affinity purification of subtypes
 CC and their histological location.

XX SQ Sequence 511 AA;

Query Match 67.2%; Score 1816.5; DB 18; Length 511;
 Best Local Similarity 68.8%; Pred. No. 4.5e-172;
 Matches 342; Conservative 56; Mismatches 94; Indels 5; Gaps 4;

QY 8 VMLAALASLLHVSILQGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSLQIMQVDE 67
 DB 16 LMASLFLSPFKVQQGSGQRRLYDLNRYNRLRPVNDSPQIVLQSLQIIVDE 75
 QY 68 KNOVLTTNIWLQMSWTQHYLQWNVSEYPGVKTVPFQDQIWKPDILLVNSADERFATFH 127
 DB 76 KNOVLITNAWLQWVVDIYLSWDQYEPGVQNLRFPSDQIWPDPILLVNSADERFATFH 135
 QY 128 TNLVNSGHQVLPQGIKSSCYIDVRWPFQVHCKLKFGSWSYGWSLQDQOEADI 187
 DB 136 TNLVNSGSCQIIPGILKSTCYIDVRWPFQVHCKLKFGSWTHSGWLDLQMLEADI 195
 QY 188 SGVIPNGEWDLVGIPGKRSEFYECCKEPEYDPDVTFTVMRRRTLYYGLNLLIPCVLISAL 247
 DB 196 SNYISNGEWDLVGVPGRKNLYEYECCKEPEYDPDVTFTVMRRRTLYYGLNLLIPCVLISGL 255
 QY 248 ALLVFLPADSGKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASITMIVGLS 307
 DB 256 ALLVFLPADSGKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASITMIVGLS 315
 QY 308 VVTVIVLQVHHDDPDGKMPKTRVILLNWCWFLMRKRPGEKVRP-ACQHK--QRRC 364
 DB 316 VVTVIVLQVHHDDPDGKMPKTRVILLNWCWFLMRKRPGEKVRP-IRPLSKSYSPKHP 374
 QY 365 SLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPHDEHLLHG 424
 DB 375 SLKNTENVLPGHQPSNGNIY-SYHTMENPCPCPNNDLGSKGITCPLSEDNHVRQK 433
 QY 425 QPPEGDPDLAKILEEYRIANRRCODESAVCESEWKAACVVDRLCIMAQSVFTICTI 484
 DB 434 ALMDTTPVIVKILEEVQFIAMRFRKDEGEICSEWKAFAAVIDRLCLVAFTLFAICTF 493
 QY 485 GILMSAPNFVAVSKDF 501
 DB 494 TILMSAPNFIEAVSKDF 510

RESULT 12
 AAB50014
 ID AAB50014 standard; Protein; 470 AA.

XX AC AAB50014;

XX DT 14-MAR-2001 (first entry)

XX DE Chimeric alpha7/5-HT3 ligand gated ion channel.

XX KW Murine; alpha7 nicotinic acetylcholine gated ion channel; human;
 XX LW 5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutant.

XX OS Chimeric - Mus musculus.

XX OS Chimeric - Homo.sapiens.

XX PN WO2000073431-A2.

XX PD 07-DEC-2000.

XX PF 25-MAY-2000; 2000WO-US11862.

XX PR 27-MAY-1999; 99US-0136174.

XX XX

PA (PHAA) PHARMACIA & UPJOHN CO.

PI Groppi VE, Wolfe ML, Berkenpas MB;

DR WPI; 2001-061524/07.

DR N-PSDB; AAC90382.

PT Special cell culture medium for treating cells and for inducing
 PT mammalian cell lines to conduct calcium ions, comprising specified
 PT concentrations of ions of sodium, calcium and potassium at specified pH

XX Claim 97; Pages 66-68; 77pp; English.

CC The present sequence is a chimeric human alpha7 nicotinic
 CC acetylcholine/murine 5-hydroxytryptamine (5-HT3) ligand gated ion
 CC channel. The alpha7/5-HT3 chimeric ion channel can be expressed by
 CC recombinant cells in the present invention, resulting in preferential
 CC calcium ion conductance by the cells.

XX SQ Sequence 470 AA;

Query Match 54.6%; Score 1474.5; DB 22; Length 470;
 Best Local Similarity 58.7%; Pred. No. 5.2e-138;
 Matches 294; Conservative 46; Mismatches 94; Indels 67; Gaps 9;

QY 1 MRCSPGGVWLAALASLLHVSILQGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSL 60

DB 1 MRCSPGGVWLAALASLLHVSILQGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSL 60

QY 61 QIMDVEDKQVLTNIWLQMSWTQHYLQWNVSEYPGVKTVPFQDQIWKPDILLVNSADE 120

DB 61 QIMDVEDKQVLTNIWLQMSWTQHYLQWNVSEYPGVKTVPFQDQIWKPDILLVNSADE 120

QY 121 RFDATFTNLVNSGHQVLPQGIKSSCYIDVRWPFQVHCKLKFGSWSYGWSLQD 180

DB 121 RFDATFTNLVNSGHQVLPQGIKSSCYIDVRWPFQVHCKLKFGSWSYGWSLQD 180

QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPEYDPDVTFTVMRRRTLYYGLNLLIP 240

DB 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPEYDPDVTFTVMRRRTLYYGLNLLIP 240

QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300

DB 240 SIFLWVDIVGFCPLPDSGERVSFKITLLGYSVFLIIVSDTLPATI-GTPLIGYFVVC 298

QY 301 MIIVGLSVVTVIVLQVHHDDPDGKMPKTRVILLNWCWFLMRKRPGEKVRPACQHK 360

DB 299 MALLVIVSLAETIFIVRLVHKQDLQRPVDPDLRLHLVLDRIAIVLCI--GEQPM----- 348

QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPHDEHL 420

DB 349 -----AHRPPATFOAN-----KTDD-----CSGSLLPANGNHC 377

QY 421 LHGG-----QPPEGDPDLA--KILEEYRIANRRCODESAVCESEWKA 463

DB 378 SHVGGPDLEKTPRGSGPLPPPREASLAVRGLLQELSSIRHFLEKRDMEVARDLVR 437

QY 464 ACVVDR-----LCIMAFSV 477

DB 438 GYVLDRLLFRIYLLAVLAYS 458

RESULT 13

AAB50018

ID AAB50018 standard; Protein; 448 AA.

XX AC AAB50018;

XX DT 14-MAR-2001 (first entry)

XX DE Mature cell surface chimeric alpha7/5-HT3 ligand gated ion channel.

KW Murine; alpha7 nicotinic acetylcholine gated ion channel; human;
 KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutant.
 XX
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX WO200073431-A2.
 PN
 XX 07-DEC-2000.
 XX
 XX 25-MAY-2000; 2000WO-US11862.
 XX
 XX 27-MAY-1999; 99US-0136174.
 XX
 XX (PHAA) PHARMACIA & UPJOHN CO.
 XX
 XX Groppi VE, Wolfe ML, Berkenpas MB;
 XX
 XX WPI; 2001-061524/07.
 XX
 XX Special cell culture medium for treating cells and for inducing
 PT mammalian cell lines to conduct calcium ions, comprising specified
 PT concentrations of ions of sodium, calcium and potassium at specified pH
 PT
 XX
 XX Disclosure; Fig 2; 77pp; English.
 PS
 XX The present sequence is the mature cell surface form of a chimeric human
 CC alpha7 nicotinic acetylcholine/murine 5-hydroxytryptamine (5-HT3) ligand
 CC gated ion channel (the full protein sequence is given in AAB50014). The
 CC alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells
 CC in the present invention, resulting in preferential calcium ion
 CC conductance by the cells.
 XX
 XX Sequence 448 AA;
 SQ
 Query Match 50.3%; Score 1360.5; DB 22; Length 448;
 Best Local Similarity 56.8%; Pred. No. 1.1e-126;
 Matches 272; Conservative 46; Mismatches 94; Indels 67; Gaps 9;
 QY 23 GEFQRLYKELVKNYPLERPVANDSQPLTVYFSLSLQIMDVDEKNQVLTNTIWLQMSW 82
 Db 1 GEFQRLYKELVKNYPLERPVANDSQPLTVYFSLSLQIMDVDEKNQVLTNTIWLQMSW 60
 QY 83 TDHYLQNVSEYPCVKTVPDQGIWKPDILLVNSADERTFTNTVLSNGHCQYLP 142
 Db 61 TDHYLQNVSEYPCVKTVPDQGIWKPDILLVNSADERTFTNTVLSNGHCQYLP 120
 QY 143 PGIFKSCYIDVRWFPDQVCKLKFGSWSGSLDLQMOEADISGYPNGEWDLVGIP 202
 Db 121 PGIFKSCYIDVRWFPDQVCKLKFGSWSGSLDLQMOEADISGYPNGEWDLVGIP 180
 QY 203 GKSERFYECKEYPDVTFTVTRRTLYYGLNLLIPCVLISALALLVFLPADSGEKI 262
 Db 181 GKSERFYECKEYPDVTFTVTRRTLYYGLNLLIPCVLISALALLVFLPADSGERV 239
 QY 263 SLGITVLLSUTTEMLVAETMPATSDVPLIAQYFASPMIIVGLSVVTVIVLQYHHDP 322
 Db 240 SFKITLLGYSVFIIIVSDTLPATI-GTPLIGVYFVCMALLVSLAETIFIVRLVHKOD 298
 QY 323 DGGMPKQWTVILLNCAWFLMRKPGEDKVRPACQHKQRCSLASVEMSAVAPPASNG 382
 Db 299 LQRPVDPWLRLVLDRIAAILCL--GEQPM-----AHRPPATFQA 336
 QY 383 NLLYIGFRGLDVHCVTPDPSGVVCGRMACSPTHDEHLLHGG-----QPP 427
 Db 337 N-----KTDDD--CSGDLPLPANGNCHSHVGGQDLEKTRGRGSLPP 377
 QY 428 EGDPDLA--KILEVRVIANFRQDESEAVCSWKFACVVD-----LCLMAFSV 477
 Db 378 PREASLAVRGILLOELSSIRHLEKRDREMRVARDWLVRGVYLDRLLFRIYLLAVLAYS 436

RESULT 14
 AAY50816
 ID AAY50816 standard; Protein; 501 AA.
 XX
 AC AAY50816;
 XX
 DT 17-FEB-2000 (first entry)
 XX
 DE H. virescens acetyl-choline receptor protein from clone Hva7-2.
 XX
 KW Acetyl-choline receptor; nicotinic; insect; insecticide; screening;
 KW neurotransmission; plant protection agent; conductance; ACHR.
 XX
 OS Heliothis virescens.
 XX
 PN DE19819829-A1.
 XX
 PD 11-NOV-1999.
 XX
 XX 04-MAY-1998; 98DE-1019829.
 XX
 XX 04-MAY-1998; 98DE-1019829.
 XX
 XX (FARB) BAYER AG.
 XX
 XX Adamczewski M, Oellers N, Schulte T;
 XX
 XX WPI; 2000-014207/02.
 XX
 XX N-PSDB; AAZ24477.
 XX
 PT New nucleic acid encoding a nicotinic acetylcholine receptor from
 PT insects, used to identify potential insecticides
 XX
 XX Example 1a; Page 22-23; 26pp; German.
 XX
 CC This invention describes a novel nucleic acid (NA) encoding a nicotinic
 CC acetyl-choline receptor (I) from insects which can be used as an
 CC insecticide. Inhibitors of (I) interfere with neurotransmission. (I)
 CC (also vectors containing it, its regulatory regions, and antibodies
 CC directed against (I)-encoded proteins) are used to screen for: (a) plant
 CC protection agents that alter conductance of ACHR, potentially useful as
 CC insecticides, or (b) genes which encode polypeptides that are involved in
 CC formation of functionally related ACHR in insects. (I) are also used to
 CC isolate and characterize the specified regulatory regions and for
 CC recombinant production of (II). This sequence represents an
 CC acetyl-choline receptor isolated from Heliothus virescens.
 XX
 SQ Sequence 501 AA;
 Query Match 46.4%; Score 1254.5; DB 21; Length 501;
 Best Local Similarity 48.4%; Pred. No. 5e-116;
 Matches 249; Conservative 75; Mismatches 139; Indels 51; Gaps 7;
 QY 10 LALAASLIHVSLOQEFQKLYKLVKNYPLERPVANDSQPLTVYFSLSLQIMDVDEKN 69
 Db 8 LALLA-LLPVSEQSPHEKRLNALLANYTLERPVANESPELVRFGLTLOQIIDVDEKN 66
 QY 70 QVLTNTIWLQMSWTDHYLQNVSEYPCVKTVPDQGIWKPDILLVNSADERTFTNT 129
 Db 67 QLLITNIWLSLEWYNDYLNWNSDEYGGVKDLRITPNKLVKPDVLMYNSADEGFDGTYQTN 126
 QY 130 VLVNSSGHCOYLPQIFKSSCYIDVRWFPDQVCKLKFGSWSGSLDLQMOE---AD 186
 Db 127 VVNRSGSCLVPPGIFKSTCKMDIAFPFDDQCHDMKFGSWTYDGNLDLVKDEAGD 186
 QY 187 ISGYIPNGEWDLVGIPGKRSEFYECKEYPDVTFTVTRRTLYYGLNLLIPCVLISA 246
 Db 187 LSDFITNGEWLIGWPGKKNITTYACCEPYVDVTFIMIRRTLYYFENLVPCVLIS 246
 QY 247 LALLVFLPADSGEKISGITVLLSUTTEMLVAETMPATSDVPLIAQYFASPMIIVGL 306
 Db 247 MALLGFTLPDPSGEEKLTGLVTILLSLTVFLNLVAETLPOVSDAIPLLGTGFNCIMFVAS 306

Qy	307	SVVTVIVLYQHHPDDGGGKPKWTRVILLNWCANFLRMKRGECKVRPACQHKQRCSL	366
Db	307	SVVLVTVVLYNHHRTADIEHPQWIKSVFLQLPWILRMRSRPGKTIIRKTIIMNTRMREL	366
Qy	367	ASVMSAVA-----PPP---ASNGNLLYIGFRGLDGVHCVPPTDGGVVC	407
Db	367	ELKERSKSLLANVLIDDDFRHGPPPPNSTATGNL-----GPGC	407
Qy	408	G-----RMACSPTHDEHLHGPGGPEGDPLAKILEEVRYIANRFRQDESEAVCSSEW	460
Db	408	SIFRDFRRSFVRPSTMEDV--GGGLGSHHRELHLILRELQFITARMKKADEAEALISDW	465
Qy	461	KPAACVDRCLCMAFSVFTIICTIGILMSAPNFV	494
Db	466	KFAAMVDRFCLEFVETLTIATVAVLISAPHII	499

RESULT 15

AAAY50815	
ID	AAAY50815 standard; Protein; 496 AA.
XX	
AC	AAAY50815;
XX	
DT	17-FEB-2000 (first entry)

DE H. virescens acetylcholine receptor protein from clone Hva7-1.

Acetyl-choline receptor; nicotinic; insect; insecticide; screening;
KW
neurotransmission; plant protection agent; conductance; AChR.
KW

AA
OS Heliothis virescens.

XX PN DE19819829-A1-

XX
11-NOV-1999XX
DE 04-MAY-1988. 88DE-1018838XX
04 MAY 1968
0000 1010000

XX

XX
PI Adamczewski M, Oellers N, Schulte T;

WPI: 2000-014207/02.

DR N-PSDB; AAZ244/6
XX

PT New nucleic acid encoding a nicotinic acetylcholine receptor from
PT insects, used to identify potential insecticides -
PT

PS Example 1a; Page 17-19; 26pp; German.

This invention describes a novel nucleic acid (NA) encoding a nicotinic acetylcholine receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence represents an acetylcholine receptor isolated from *Heliothius virescens*.

Sequence 496 AA;

Query Match 45.9%; Score 1242; DB 21; Length 496;

Best local similarity 45.8%; Pred. NO. 8./e-113;
Matches 239: Conservative 86: Mismatches 127:

4. SPENDING AT A TAXI Y UNIT OCCURRED AT THE FOLLOWING PLACES:

[illegible]

Qy	64	DVDEKNQVLTTNIWLOMSWTDHYIOWNVSEYFGUKTVTFPDGOIWKPDILLVNSADERPD	123
Db	72	DVDEKNQLLITNIWLOKEWDMNIRWNTSDFGGKUEWLPVPHRLWKPDVLWYNSADEGFD	131
Qy	124	ATFTHTNVLVNSSGHGCOYLPPGCIKFSSCSVIDVRWPFVDVQHCKLKFSGMSYGGWSLDLOMQ	183
Db	132	STYFTNVVRNNGSLVYPPGCIFASTCKIDITWPFDDQRCMEKFGSWTYDGYQLDLQLO	191
Qy	184	E---ADISGYIPNGEWDLVGIPGKRBRFYECCKEPPYDPDVTFTVTMRRTLLYYGUNLLIP	240
Db	192	DEGGDISSFVTNGEWEELIVPGFGKRNETIYNCCPEPYIDITFAVVIRBKTYFFFNLIYP	251
Qy	241	CVLISALALLVFLLPADSGEKISAGITVLLSLTTFMLLVASIMPATSDSVPLIAOYFAST	300
Db	252	CVLIASHALLGFTLPPDSGEKLSUGVTILLSTTVFLNVAETMPATSDAVPLUGYFNCI	311
Qy	301	MIIVGLSGVVTVIVLOVHHHDPDGGKMPKWTFRVILLNCAWFLMRKRPGEKVRPACQHK	360
Db	312	MFVASSVSVSTILINTVHRRHADTHEMSDWIRCVFLYWL PWVLRMSRPG-----	360
Qy	361	QRRCSLASVEMSAVAPPASNGNLLYITGFRGLDGVHCVPTPDSGVVCGRMACSPTH----	416
Db	361	-----SATTPPPAR-----VPPPDLELRERSKSLLANVLD	392
Qy	417	-DEHLH-----GGQPEG-----DPDLAKLILEEVRVYIANRPERCODE	452
Db	393	IDDDFRHPQAOQCCRYRGGEEENGAGLAHSCFGVDYELSLILKEIRVITDQMRKDE	452
Qy	453	SEAVCSBWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNJV	494
Db	453	DADISRDWKFAAMVVDRLCLIIIFLTITATLAVLLSAPHIM	494

Search completed: June 20, 2003, 18:58:22
Job time : 76 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2003, 19:07:31 ; Search time 82 Seconds
(without alignments)
1261.410 Million cell updates/sec

Title: US-09-954-936-2
Perfect score: 502
Sequence: 1 WRCSGCVWLALAAALLHVS.....TIGILMSAPNFVEAVSKDFA 502

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 6

Total number of hits satisfying chosen parameters: 6089

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	17.3	157	6	Q9TUL2
2	68	13.5	68	6	Q9TUC7
3	62	12.4	502	11	Q9JHD6
4	46	9.2	86	13	Q90XF5
5	37	7.4	65	11	Q9EPU9
6	34	6.8	115	11	Q8VI09
7	27	5.4	511	13	Q03481
8	12	2.4	573	5	Q9GQU9
9	11	2.2	500	5	Q22224
10	10	2.0	134	11	Q99MD4
11	10	2.0	477	11	Q62999
12	10	2.0	483	6	Q9N0F4
13	10	2.0	484	4	Q9BS29
14	10	2.0	484	11	O70213
15	10	2.0	490	11	O70212
16	10	2.0	510	4	O60854

17	10	2.0	542	5	Q18556
18	9	1.8	291	16	Q98L83
19	9	1.8	426	5	Q96760
20	9	1.8	447	11	Q9JLB5
21	9	1.8	473	5	Q94789
22	9	1.8	484	13	Q9PTS8
23	9	1.8	510	5	Q21645
24	9	1.8	512	5	Q92039
25	9	1.8	545	5	Q96631
26	9	1.8	580	5	Q9VC72
27	8	1.6	49	5	Q9NIU9
28	8	1.6	113	10	Q40329
29	8	1.6	113	10	Q40330
30	8	1.6	245	16	O25463
31	8	1.6	248	5	O02399
32	8	1.6	301	12	Q91B08
33	8	1.6	301	12	Q9E225
34	8	1.6	452	13	Q918C7
35	8	1.6	452	16	Q916J3
36	8	1.6	458	17	Q8TVI3
37	8	1.6	461	5	P91197
38	8	1.6	515	2	Q8VPP9
39	8	1.6	515	5	O16926
40	8	1.6	531	5	Q96632
41	8	1.6	533	5	Q8WRS1
42	8	1.6	552	5	Q9VC74
43	8	1.6	554	5	O62083
44	8	1.6	707	16	Q98JV6
45	8	1.6	974	11	Q924W2

ALIGNMENTS

RESULT 1

Q9TUL2 ID Q9TUL2 PRELIMINARY; PRT; 157 AA.
AC Q9TUL2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Nicotinic acetylcholine receptor subunit alpha7 (Fragment).
OS NICA7.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=20485464; PubMed=11029636;
RA Han Z.Y., Le Novere N., Zoli M., Champiaux N., Hill J.A.,
RA Changeux J.P.;
RT "Localization of nAChR subunit mRNAs in the brain of Macaca mulatta.";
RL Eur. J. Neurosci. 12:3664-3674(2000).
DR EMBL; AJ245976; CAB53253.1;
DR InterPro; IPR00188; GABAA_receptor.
DR FT NON TER 1
FT NON TER 157
SQ SEQUENCE 157 AA; 17411 MW; C78A5989A964BE26 CRC64;

Query Match 17.3%; Score 87; DB 6; Length 157;
Best Local Similarity 100.0%; Pred.No. 2.4e-82;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 409 RMACSPHDEHLLGGPPGPDPLAKILEVRYIANFRQDESEAVCSWKAACVVD 468
Db 71 RMACSPHDEHLLGGPPGPDPLAKILEVRYIANFRQDESEAVCSWKAACVVD 130
Qy 469 RLCLMAFSVFTIITIGILMSAPNFVE 495


```
DB 131 RLCLMAFSVFTICTIGILMSAPNFV 157
|||||
RESULT 2
Q9TUC7 PRELIMINARY; PRT; 68 AA.
AC Q9TUC7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Nicotinic acetylcholine receptor alpha 7 subunit (Fragment).
OS Nicotiana glauca (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Sekhon H.S., Jia Y., Raab R., Kuryatov A., Pankow J.F., Whitsett J.A.,
RA Lindstrom J., Spindel E.R.;
RT "prenatal nicotine exposure increases alpha 7 nicotinic acetylcholine
RT receptor expression in pulmonary cells and alters fetal lung
RT development in monkeys.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF087689; AAF02221.1;
DR InterPro; IPR000188; GABAA_receptor.
DR Pfam; PF02932; Neur_chan_memb; 1.
KW Receptor.
FT NON_TER
SQ SEQUENCE 68 AA; 7700 MW; B18048F0948B6477 CRC64;
Query Match 13.5%; Score 68; DB 6; Length 68;
Best Local Similarity 100.0%; Pred. No. 8.5e-63;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 435 KILEEVRYIANRRCQDESEAVSEWKFACVVDRLCLMAFSVFTICTIGILMSAPNFV 494
|||||
DB 1 KILEEVRYIANRRCQDESEAVSEWKFACVVDRLCLMAFSVFTICTIGILMSAPNFV 60
QY 495 EAVSKDFA 502
|||||
DB 61 EAVSKDFA 68
RESULT 3
Q9JHD6 PRELIMINARY; PRT; 502 AA.
AC Q9JHD6
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Nicotinic acetylcholine receptor subunit alpha 7.
GN CHRNA7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=DBA/21BG;
RX MEDLINE=97189245; PubMed=9037516;
RA Stitzel J.A., Farnham D.A., Collins A.C.;
RT "Linkage of strain-specific nicotinic receptor alpha 7 subunit
RT restriction fragment length polymorphisms with levels of alpha-
RT bungarotoxin binding in brain.";
RL Brain Res. Mol. Brain Res. 43:30-40 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=DBA/21BG;
RA Stitzel J.A.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1, SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL; AF225980; AAF35885.1;
DR MGD; MGI:99779; Chnra7.
DR InterPro; IPR000188; GABAA_receptor.
DR InterPro; IPR001175; Neur_channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
SQ SEQUENCE 502 AA; 56617 MW; C9353E5136D620E3 CRC64;
Query Match 12.4%; Score 62; DB 11; Length 502;
Best Local Similarity 100.0%; Pred. No. 9.3e-56;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 LYKELVKNYNPLERPANDSQPLTVYFSLSLQIMDVDEKQVLTNNIWLQMSWDHYLQ 88
|||||
DB 29 LYKELVKNYNPLERPANDSQPLTVYFSLSLQIMDVDEKQVLTNNIWLQMSWDHYLQ 88
QY 89 WN 90
|||
DB 89 WN 90
RESULT 4
Q90XF5 PRELIMINARY; PRT; 86 AA.
AC Q90XF5
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Neuronal nicotinic acetylcholine receptor alpha-7 chain
DE (Fragment).
OS Coturnix coturnix (common quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=9091;
RN [1]
RP SEQUENCE FROM N.A.
RA Bader A.G., Schneider M.L., Bister K., Hartl M.;
RT "TOU3, a target of the v-Jun transcription factor, encodes a protein
RT with transforming activity related to human microspherule protein 1
RT (MCRS1).";
RL Oncogene 0:0-0 (2001).
DR EMBL; AF390033; AAK73731.1;
DR InterPro; IPR000188; GABAA_receptor.
DR Pfam; PF02932; Neur_chan_memb; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 86 86
SQ SEQUENCE 86 AA; 9700 MW; 445314D42B08E4CA CRC64;
Query Match 9.2%; Score 46; DB 13; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.1e-39;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 321 DPDGKMPKWTFRVILLNCWAFRLMKRPGEDKVRPACQHKQRCSL 366
|||||
DB 1 DPDGKMPKWTFRVILLNCWAFRLMKRPGEDKVRPACQHKQRCSL 46
RESULT 5
Q9EPU9 PRELIMINARY; PRT; 65 AA.
AC Q9EPU9
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Nicotinic receptor alpha 7 subunit (Fragment).
```

```
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;
RX MEDLINE=21264418; PubMed=11278551;
RA Nagavara U., Danchi S., Boyd R.T.;
RT "Characterization of a Rat Neuronal Nicotinic Acetylcholine Receptor
RT alpha 7 Promoter.";
RL J. Biol. Chem. 276:16749-16757 (2001).
DR EMBL; AF321242; AAG39219.1; -.
DR InterPro; IPR001175; Neur_chan.
DR Pfam; PF02931; Neur_chan_LBD; 1.
KW Receptor.
FT NON TER
SQ SEQUENCE 65 AA; 7305 MW; 7C795E602A0CA2AB CRC64;

Query Match 7.4%; Score 37; DB 11; Length 65;
Best Local Similarity 100.0%; Pred. No. 2.2e-30;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 LYKELVKNYPLRPVANDSQPLTVYFSLQLQIMDV 65
DB 29 LYKELVKNYPLRPVANDSQPLTVYFSLQLQIMDV 65
|||||
RESULT 6
OSV109 PRELIMINARY; PRT; 115 AA.
ID Q8V109
AC Q8V109;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Nicotinic acetylcholine receptor alpha 7 subunit (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kuo Y.-P., Lukas R.J.;
RT "Expression of mouse nicotinic acetylcholine receptor genes in the
RT developing thymus.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF325348; AAL37364.1; -.
DR InterPro; IPR001175; Neur_chan.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; UNKNOWN_1.
KW Receptor.
FT NON TER
FT NON TER
SQ SEQUENCE 115 AA; 13586 MW; 45D637A1FF6E7CA7 CRC64;

Query Match 6.8%; Score 34; DB 11; Length 115;
Best Local Similarity 100.0%; Pred. No. 4.9e-27;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 VRFPDQIQWPKDILLVNSADERPDFTHTNLVYN 133
DB 49 VRFPDQIQWPKDILLVNSADERPDFTHTNLVYN 82
|||||
RESULT 7
Q03481 PRELIMINARY; PRT; 511 AA.
ID Q03481
AC Q03481;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
```

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DE Alpha8 subunit of nicotinic acetylcholine receptor precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae; Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=90311518; PubMed=2369519;
RA Schoeffer R., Conroy W.G., Whiting P., Gore M., Lindstrom J.;
RT "Brain alpha-bungarotoxin-binding protein cDNAs and mABs reveal
RT subtypes of this branch of the ligand-gated ion channel gene
RT superfamily.";
RL Neuron 5:35-48 (1990).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL; X52296; CAA36544.1; -.
DR InterPro; IPR000188; GABAA_receptor.
DR InterPro; IPR001175; Neur_chan.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor; Signal; Transmembrane.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 511 POTENTIAL.
SQ SEQUENCE 511 AA; 58705 MW; 10F362D153EC87A7 CRC64;

Query Match 5.4%; Score 27; DB 13; Length 511;
Best Local Similarity 100.0%; Pred. No. 3.8e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 LALLVFLPADSGEKISLGITVLLSLT 273
DB 255 LALLVFLPADSGEKISLGITVLLSLT 281
|||||
RESULT 8
Q9GQU9 PRELIMINARY; PRT; 573 AA.
ID Q9GQU9
AC Q9GQU9; Q21615;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Nicotinic acetylcholine receptor-like subunit ACR-12 (R01E6.4
DE protein).
DE R01E6.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N2;
RX MEDLINE=9200102; PubMed=10100329;
RA Mongan N.P., Baylis H.A., Adcock C., Smith G.R., Sansom M.S.,
RA Sattelle D.B.;
RT "An extensive and diverse gene family of nicotinic acetylcholine
RT receptor alpha subunits in Caenorhabditis elegans.";
RL Recept. Channels 6:213-228 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=N2;
RA Mongan N.P., Gower N.J.D., Culetto E., Sattelle D.B.;
RT "Isolation and characterization of two novel nicotinic acetylcholine
RT receptor alpha subunit encoding cDNAs from the nematode,
RT Caenorhabditis elegans.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
```

RA Coles L.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN (4)
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology."
RL Science 282:2012-2018(1998).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL; AF187013; AAG35183.1; -.
DR EMBL; Z68118; CAA92184.2; -.
DR InterPro; IPR001188; GABAA_receptor.
DR InterPro; IPR001175; Neur_chan_LBD; 1.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
Transmembrane.
SQ SEQUENCE 573 AA; 65707 MW; 5CFBACF3903548B2 CRC64;

Query Match 2.4%; Score 12; DB 5; Length 573;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 DVDEKNQVLTTN 75
| | | | | | | | | |
DB 76 DVDEKNQVLTTN 87

RESULT 9
Q22224
ID Q22224 PRELIMINARY; PRT; 500 AA.
AC Q22224;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE T05C12.2 protein.
GN T05C12.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN (1)
RP SEQUENCE FROM N.A.
RA Burton J.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology."
RL Science 282:2012-2018(1998).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL; Z66500; CAA91304.2; -.
DR InterPro; IPR002106; AATRNA_ligaseII.
DR InterPro; IPR000188; GABAA_receptor.
DR InterPro; IPR001175; Neur_chan_LBD; 1.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Transmembrane.
SQ SEQUENCE 500 AA; 57675 MW; 20BD4CBF19614892 CRC64;
Query Match 2.2%; Score 11; DB 5; Length 500;
Best Local Similarity 100.0%; Pred. No. 0.02;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 61 QIMDVDEKNQV 71
| | | | | | | | | |
DB 56 QIMDVDEKNQV 66
RESULT 10
Q99MD4
ID Q99MD4 PRELIMINARY; PRT; 134 AA.
AC Q99MD4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Acetylcholine receptor alpha 9 subunit (Fragment).
GN NACHR.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN (1)
RP SEQUENCE FROM N.A.
RA He D.Z., Zheng J., Dallos P.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF350252; AAK29438.1; -.
DR InterPro; IPR000188; GABAA_receptor.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR Receptor.
KW NON TER 1 1
FT NON TER 134 134
SQ SEQUENCE 134 AA; 14779 MW; 74925CD3D70C8999 CRC64;

Query Match 2.0%; Score 10; DB 11; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 236 NLLIPCVLIS 245
| | | | | | | | | |
DB 5 NLLIPCVLIS 14

RESULT 11
Q62999
ID Q62999 PRELIMINARY; PRT; 477 AA.
AC Q62999;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE SHT3 receptor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RA Johnson D.S.;
RL "Rat SHT3 receptor sequence."
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL; U59672; AAB02949.1; -.
DR InterPro; IPR000188; GABAA_receptor.
DR InterPro; IPR001175; Neur_chan_LBD; 1.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
Transmembrane.
SQ SEQUENCE 477 AA; 54837 MW; 3DCCFC34F175FCC3 CRC64;

Query Match 2.0%; Score 10; DB 11; Length 477;
 Best Local Similarity 100.0%; Pred. No. 0.22; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 VDEKNQVLTT 74
 |||||
 Db 72 VDEKNQVLTT 81

RESULT 12

ID Q9N0F4 PRELIMINARY; PRT; 483 AA.
 AC Q9N0F4
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Ferret 5-HT3A receptor.
 OS Mustela putorius furo (Ferret).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
 OC Mustela.
 OX NCBI_TaxID=9669;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=COLON;
 RX MEDLINE=20344772; PubMed=10884508;
 RA Mochizuki S., Watanabe T., Miyake A., Saito M., Furuichi K.;
 RT "Cloning, expression, and characterization of ferret 5-HT3 receptor subunit";
 RL Eur. J. Pharmacol. 399:97-106(2000).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
 DR EMBL; AB029898; BAA96417.1; -.
 DR InterPro; IPR001188; GABAA receptor.
 DR InterPro; IPR001175; Neur. Channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMS; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
 KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
 KW Transmembrane.
 SQ SEQUENCE 483 AA; 55562 MW; 54695AC794E30206 CRC64;

Query Match 2.0%; Score 10; DB 6; Length 483;
 Best Local Similarity 100.0%; Pred. No. 0.22; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 VDEKNQVLTT 74
 |||||
 Db 78 VDEKNQVLTT 87

RESULT 13

ID Q9BSZ9 PRELIMINARY; PRT; 484 AA.
 AC Q9BSZ9
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical 55.9 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
 DR EMBL; BC004453; AA044453.1; -.

DR InterPro; IPR000188; GABAA receptor.
 DR InterPro; IPR001005; Myb_DNA_binding.
 DR InterPro; IPR001175; Neur_channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMS; TIGR00860; LIC; 1.
 DR PROSITE; PS00334; MYB 2; UNKNOWN 1.
 DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
 KW Glycoprotein; Hypothetical protein; Ionic channel;
 KW Postsynaptic membrane; Transmembrane.
 SQ SEQUENCE 484 AA; 55894 MW; 74F70567007BCB51 CRC64;

Query Match 2.0%; Score 10; DB 4; Length 484;
 Best Local Similarity 100.0%; Pred. No. 0.22;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 VDEKNQVLTT 74
 |||||
 Db 79 VDEKNQVLTT 88

RESULT 14

ID O70213 PRELIMINARY; PRT; 484 AA.
 AC O70213
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE 5-HT3-As receptor precursor.
 GN 5-HT3.
 OS Cavia porcellus (Guinea pig);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=INTESTINE;
 RX MEDLINE=98130690; PubMed=9463477;
 RA Laukiewicz S., Lobitz N., Wetzel C.H.R., Rupprecht R., Gisselmann G.,
 Hatt H.;
 RT "Molecular cloning, functional expression, and pharmacological characterization of 5-hydroxytryptamine3 receptor cDNA and its splice variants from guinea pig";
 RL Mol. Pharmacol. 53:202-212(1998).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
 DR EMBL; AF006462; AAC06137.1; -.
 DR InterPro; IPR000188; GABAA receptor.
 DR InterPro; IPR001175; Neur_Channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMS; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
 KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor; Signal;
 KW Transmembrane.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 484 5-HT3-AS RECEPTOR.
 SQ SEQUENCE 484 AA; 55087 MW; F7CF69D582ADB82 CRC64;

Query Match 2.0%; Score 10; DB 11; Length 484;
 Best Local Similarity 100.0%; Pred. No. 0.22;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 VDEKNQVLTT 74
 |||||
 Db 78 VDEKNQVLTT 87

RESULT 15

O70212 PRELIMINARY; PRT; 490 AA.
 ID O70212

AC 070212;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE 5-HT3-A1 receptor precursor.
 GN 5-HT3.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OC NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=INTESTINE;
 RX MEDLINE=98130690; PubMed=9463477;
 RA Lankiewicz S., Lobitz N., Wetzel C.H.R., Rupprecht R., Gisselmann G.,
 RA Hatt H.;
 RT "Molecular cloning, functional expression, and pharmacological
 RT characterization of 5-hydroxytryptamine3 receptor cDNA and its splice
 RT variants from guinea pig.";
 RL Mol. Pharmacol. 53:202-212(1998).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
 DR EMBL; AF006461; AAC06136.1; -.
 DR InterPro; IPR000188; GABAA_receptor.
 DR InterPro; IPR001175; Neur_Channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NR1ONCHANNEL.
 DR TIGRPFAM; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor; Signal;
 KW Transmembrane.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 490 5-HT3-AL RECEPTOR.
 SQ SEQUENCE 490 AA; 53655 MW; EDB32F8597494F61 CRC64;

Query Match 2.0%; Score 10; DB 11; Length 490;
 Best Local Similarity 100.0%; Pred. No. 0.22;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 VDEKNQVLTT 74
 |||||
 Db 78 VDEKNQVLTT 87

Search completed: June 20, 2003, 19:13:42
 Job time : 88 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2003, 19:01:56 ; Search time 24 Seconds
(without alignments)
867.547 Million cell updates/sec

Title: US-09-954-936-2

Perfect score: 502

Sequence: 1 MRCSPGGWLLAALSLHVS.....TIGILMSAPNFVAVSKDFA 502

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 6

Total number of hits satisfying chosen parameters: 996

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	401	79.9	502	1 ACH7 HUMAN	P36544 homo sapien
2	92	18.3	502	1 ACH7 CHICK	P22770 gallus gall
3	71	14.1	499	1 ACH7 BOVIN	P54131 bos taurus
4	62	12.4	502	1 ACH7 MOUSE	P49582 mus musculus
5	62	12.4	502	1 ACH7 RAT	Q05941 rattus norv
6	10	2.0	478	1 SHT3 HUMAN	P46098 homo sapien
7	10	2.0	479	1 ACH9 HUMAN	Q9ugml homo sapien
8	10	2.0	479	1 ACH9 RAT	P43144 rattus norv
9	10	2.0	483	1 SHT3 RAT	P35563 rattus norv
10	10	2.0	487	1 SHT3 MOUSE	P23979 mus musculus
11	9	1.8	436	1 ACHX ONCVO	P54247 onchocerca
12	9	1.8	450	1 ACHX HUMAN	Q9g226 homo sapien
13	9	1.8	498	1 ACHX CAEBL	P48180 caenorhabdi
14	9	1.8	511	1 ACH5 CAEBL	Q23022 caenorhabdi
15	9	1.8	557	1 ACH1 SCHGR	P23414 schistocerc
16	9	1.8	576	1 ACH2 DROME	P17644 drosophila
17	8	1.6	496	1 ACH3 CHICK	P09481 gallus gall
18	8	1.6	513	1 ACHD CHICK	P02717 gallus gall
19	8	1.6	517	1 ACHD HUMAN	Q07001 homo sapien
20	8	1.6	521	1 ACHD XENLA	P09628 xenopus lae
21	8	1.6	567	1 ACH1 DROME	P09478 drosophila
22	8	1.6	1072	1 ITA6 CHICK	P26007 gallus gall
23	8	1.6	1091	1 ITA6 MOUSE	Q61739 mus musculus
24	7	1.4	67	1 HMT2 METHTH	Q27731 methanobact
25	7	1.4	69	1 HMT2 METHTE	P19267 methanobact
26	7	1.4	127	1 RPOZ RICCN	Q92h89 rickettsia
27	7	1.4	144	1 PSB1 ECOLI	P10031 escherichia
28	7	1.4	144	1 PSB2 ECOLI	P10032 escherichia
29	7	1.4	174	1 CSF3 SHEEP	Q28746 ovis aries
30	7	1.4	175	1 HES3 RAT	Q04667 rattus norv
31	7	1.4	195	1 CSF3 BOVIN	P35833 bos taurus
32	7	1.4	195	1 CSF3 PIG	O02837 sus scrofa
33	7	1.4	198	1 SCP2 BACSU	P81100 bacillus su

ALIGNMENTS

RESULT 1

ID	ACH7_HUMAN	STANDARD;	PRT;	502 AA.
AC	P36544; Q15826; Q99555; Q96RH2; Q9BXH0;			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Neuronal acetylcholine receptor protein, alpha-7 chain precursor.			
GN	CHRNA7 OR NACHRA7.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=94195283; PubMed=8145738;			
RA	Peng X., Katz M., Gerzanich V., Anand R., Lindstrom J.;			
RT	"Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from the SH-SY5Y cell line and determination of pharmacological properties of native receptors and functional alpha 7 homomers expressed in Xenopus oocytes.";			
RT	Mol. Pharmacol. 45:546-554(1994).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Hippocampus;			
RA	Logel J., Drebing C., Barnhart M., Antle C., Leonard S.;			
RL	Submitted (DSC-1995) to the EMBL/GenBank/DBJ databases.			
[3]				
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=97062879; PubMed=8906617;			
RA	Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,			
RA	Chavez-Noriega L.E., Johnson E.C., Vellicolebi G., Harpold M.M.;			
RT	"Comparative structure of human neuronal alpha 2-alpha 7 and beta 2-beta 4 nicotinic acetylcholine receptor subunits and functional expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and beta 4 subunits.";			
RT	J. Mol. Neurosci. 7:217-228(1996).			
RL	[4]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=97162233; PubMed=9009220;			
RA	Groot Kormelink P.J., Luyten W.H.M.L.;			
RT	"Cloning and sequence of full-length cDNAs encoding the human neuronal Nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and expression of seven nAChR subunits in the human neuroblastoma cell line SH-SY5Y and/or IMR-32.";			
RT	FEBS Lett. 400:309-314(1997).			
RL	[5]			
RN	SEQUENCE FROM N.A.			
RP	Groot Kormelink P.J., Luyten W.H.M.L.;			
RT	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.			
RL	[6]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Epidermal keratinocytes;			
RC	Arredondo J., Grando S.A.;			
RT	"Cloning cholinergic receptors in human keratinocytes.";			

34	7	1.4	216	1	ATP6 AQUAE	O66566 aquifex aso
35	7	1.4	230	1	FLAH_METVO	O06641 mehanococc
36	7	1.4	262	1	ZNOB_BUCAL	P57402 buchnera ap
37	7	1.4	269	1	Y2B_MYCGE	Q92b74 mycoplasma
38	7	1.4	290	1	LEP_HELPJ	Q92lq5 helicobacte
39	7	1.4	290	1	LEP_HELPJ	O25300 helicobacte
40	7	1.4	316	1	Y273_SVNY3	P73894 synechocyst
41	7	1.4	321	1	SAPB_SALTY	P36668 salmonella
42	7	1.4	347	1	NU2M_RHIUN	Q96061 rhinoceros
43	7	1.4	353	1	BRB1_HUMAN	P46663 homo sapien
44	7	1.4	376	1	DXR_TREPA	O83610 treponema p
45	7	1.4	398	1	YJ16_CAUCR	Q9a710 caulobacter

Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 [7] SEQUENCE OF 17-502 FROM N.A.
 RP TISSUE=Brain;
 RA Doucette-Stamm L., Monteggia L.M., Donnelly-Roberts D., Wang M.T.,
 RA Lee J., Tian J., Giordano T.;
 RT "Cloning and sequence of the human a7 nicotinic acetylcholine
 RT receptor.";
 RL Drug Dev. Res. 30:252-256(1993).
 [8]
 RP SEQUENCE OF 24-502 FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=94245214; PubMed=8188270;
 RA Chini B., Rainondi E., Elgoyhen A.B., Moralli D., Balzaretti M.,
 RA Heinemann S.F.;
 RT "Molecular cloning and chromosomal localization of the human alpha 7-
 RT nicotinic receptor subunit gene (CHRNA7).";
 RL Genomics 19:379-381(1994).
 [9]
 RP SEQUENCE OF 118-129 FROM N.A.
 RX PubMed=11829490;
 RA Riley B., Williamson M., Collier D., Wilkie H., Makoff A.;
 RT "A 3-Mb map of a large segmental duplication overlapping the alpha7-
 RT nicotinic acetylcholine receptor gene (CHRNA7) at human 15q13-q14.";
 RL Genomics 79:197-209(2002).
 [10]
 RP MASS SPECTROMETRY.
 RC TISSUE=Breast cancer;
 RX MEDLINE=21829512; PubMed=11840567;
 RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
 RA Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
 RA Zvelebil M.J.;
 RT "Cluster analysis of an extensive human breast cancer cell line
 RT protein expression map database.";
 RL Proteomics 2:212-223(2002).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
 CC HUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
 CC SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- MASS SPECTROMETRY: MW=54157.68; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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 CC
 CC EMBL; X70297; CAA49778.1; -;
 CC EMBL; U40583; AAB93561.1; -;
 CC EMBL; U62436; AAB40114.1; -;
 CC EMBL; Y08420; CAA69697.1; -;
 CC EMBL; AF385585; AAK68111.1; -;
 CC EMBL; L25827; -; NOT ANNOTATED_CDS.
 CC EMBL; Z23141; CAA80672.1; -;
 CC EMBL; AF332758; AAK19515.1; -;
 CC Genew; HGNC:11960; CHRNA7.
 CC MIM; 118511; -;
 CC InterPro; IPR000188; GABAA_receptor.
 CC InterPro; IPR001175; Neur_Channel.
 CC Pfam; PF02931; Neur_chan_1BD; 1.
 CC Pfam; PF02932; Neur_chan_memb; 1.
 CC PRINTS; PR00252; NRIONCHANNEL.
 CC TIGRFAMs; TIGR00860; LIC; 1.
 CC PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 CC Postsynaptic membrane; Ion channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.

FT	SIGNAL	1	22	BY SIMILARITY.
FT	CHAIN	23	502	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
FT				ALPHA-7 CHAIN.
FT	DOMAIN	23	230	EXTRACELLULAR (POTENTIAL).
FT	TRANSNEM	231	255	POTENTIAL.
FT	TRANSNEM	262	280	POTENTIAL.
FT	TRANSNEM	296	317	POTENTIAL.
FT	DOMAIN	318	469	CYTOPLASMIC (POTENTIAL).
FT	TRANSNEM	470	490	POTENTIAL.
FT	DISULFID	150	164	BY SIMILARITY.
FT	DISULFID	212	213	ASSOCIATED WITH RECEPTOR ACTIVATION
FT				(BY SIMILARITY).
FT	CARBOHYD	46	46	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	90	90	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	133	133	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	11	11	A -> G (IN REF. 1 AND 7).
FT	CONFLICT	58	58	S -> N (IN REF. 2 AND 6).
FT	CONFLICT	134	134	S -> P (IN REF. 2 AND 6).
FT	CONFLICT	364	364	C -> S (IN REF. 8).
FT	CONFLICT	375	375	A -> G (IN REF. 1).
FT	CONFLICT	409	413	RMACS -> AWPAP (IN REF. 8).
FT	SEQUENCE	502 AA;	56449 MW;	D94B3A482EAA0E42 CRC64;
QY	1	MRCS	PGVWLAALASLLHVS	LGQEFQRLKYLKYNYNPLRPVANDSQPLTVVFSLSLL 60
DB	1	MRCS	PGVWLAALASLLHVS	LGQEFQRLKYLKYNYNPLRPVANDSQPLTVVFSLSLL 60
QY	61	QIMD	VDEKNOVLTNINLQMS	WTDHYLQMNVSYPGVKTVRFPGQIWKPDILLVNSADE 120
DB	61	QIMD	VDEKNOVLTNINLQMS	WTDHYLQMNVSYPGVKTVRFPGQIWKPDILLVNSADE 120
QY	121	RFDA	TFTNVLNVS	SGHCQYLPPGIFKSSCYIDVRWFPFDVQHCKLFGSGWSJDL 180
DB	121	RFDA	TFTNVLNVS	SGHCQYLPPGIFKSSCYIDVRWFPFDVQHCKLFGSGWSJDL 180
QY	181	QMQA	DISGYIPNGE	WDLVIGPKRSERFECCKEYPDVTFTVMRRRTLYYGLNLLIP 240
DB	181	QMQA	DISGYIPNGE	WDLVIGPKRSERFECCKEYPDVTFTVMRRRTLYYGLNLLIP 240
QY	241	CVLS	ALALLVFLPAD	SGEKISIGITVLLSLTTFMLVAEIMPATSDSVPLIAQYFAS 300
DB	241	CVLS	ALALLVFLPAD	SGEKISIGITVLLSLTTFMLVAEIMPATSDSVPLIAQYFAS 300
QY	301	MIIV	GLSVVTVIVLQY	HHDDPDGGMKPKWTRVILLNWCANFLMRKRPGEKVRPACQHK 360
DB	301	MIIV	GLSVVTVIVLQY	HHDDPDGGMKPKWTRVILLNWCANFLMRKRPGEKVRPACQHK 360
QY	361	QRRCS	LASVEMSAVAPP	ASNGNLLYIGFRLDGVCHVCTPTDPSGVVCGRMACSPTHDHL 420
DB	361	QRRCS	LASVEMSAVAPP	ASNGNLLYIGFRLDGVCHVCTPTDPSGVVCGRMACSPTHDHL 420
QY	421	LHGG	OPPEGDDIAKIL	EEVRYIANRRCQDESEAVCSEWKFACVVDRLCLMAFSVFTI 480
DB	421	LHGG	OPPEGDDIAKIL	EEVRYIANRRCQDESEAVCSEWKFACVVDRLCLMAFSVFTI 480
QY	481	ICTI	GILMSAPNFVEA	VSCKDFA 502
DB	481	ICTI	GILMSAPNFVEA	VSCKDFA 502

Query Match 79.9%; Score 401; DB 1; Length 502;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 2
 ACH7 CHICK
 ID -ACH7 CHICK STANDARD; PRT; 502 AA.
 AC P22770;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
 OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RC MEDLINE=91097796; PubMed=1702646;
 RX Couturier S., Bertrand D., Matter J.M., Hernandez M.C., Bertrand S.,
 RA Millar N., Valera S., Barkas T., Ballivet M.;
 RA "A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is
 RT developmentally regulated and forms a homo-oligomeric channel blocked
 RT by alpha-BTX.";
 RL Neuron 5:847-856(1990).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RC MEDLINE=90315158; PubMed=2369519;
 RX Schoepfer R., Conroy W.G., Whiting P., Gore M., Lindstroem J.;
 RA "Brain alpha-bungarotoxin binding protein cDNAs and MABs reveal
 RT subtypes of this branch of the ligand-gated ion channel gene
 RT superfamily.";
 RL Neuron 5:35-48(1990).
 RN [3]
 RN SEQUENCE OF 1-18 FROM N.A.
 RP STRAIN=White leghorn; TISSUE=Erythrocyte;
 RC MEDLINE=93049204; PubMed=1425587;
 RX Matter-Sadzinski L., Hernandez M.C., Rottocil T., Ballivet M.,
 RA Matter J.M.;
 RA "Neuronal specificity of the alpha 7 nicotinic acetylcholine receptor
 RT promoter develops during morphogenesis of the central nervous
 RT system.";
 RL EMBO J. 11:4529-4538(1992).
 RN [4]
 RN SEQUENCE OF 24-47.
 RP TISSUE=Brain;
 RC MEDLINE=85270494; PubMed=3860855;
 RX Conti-Tronconi B.M., Dunn S.M.J., Barnard E.A., Dolly J.O., Lai F.A.,
 RA Ray N., Raftery M.A.;
 RA "Brain and muscle nicotinic acetylcholine receptors are different but
 RT homologous proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:5208-5212(1985).
 RN [5]
 RN MUTAGENESIS OF LEU-270.
 RP MEDLINE=92049732; PubMed=1719423;
 RX Recah F., Bertrand D., Galzi J.-L., Devillers-Thiery A., Mulle C.,
 RA Hussy N., Bertrand S., Ballivet M., Changeux J.-P.;
 RA "Mutations in the channel domain alter desensitization of a neuronal
 RT nicotinic receptor.";
 RL Nature 353:846-849(1991).
 RN [6]
 RN MUTAGENESIS TO CONVERT ION SELECTIVITY FROM CATIONIC TO ANIONIC.
 RP MEDLINE=93024917; PubMed=1383929;
 RX Galzi J.-L., Devillers-Thiery A., Hussy N., Bertrand S.,
 RA Changeux J.-P., Bertrand D.;
 RA "Mutations in the channel domain of a neuronal nicotinic receptor
 RT convert ion selectivity from cationic to anionic.";
 RL Nature 359:500-505(1992).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
 CC BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
 CC SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- DEVELOPMENTAL STAGE: ALPHA-7 TRANSCRIPTS TRANSIENTLY ACCUMULATE
 CC IN THE DEVELOPING OPTIC TECTUM BETWEEN E5 AND E16.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC
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 CC -----
 DR EMBL; X52295; CAA36543.1; -;
 DR EMBL; X68246; CAA48317.1; -;
 DR EMBL; X68586; CAA48576.1; -;
 DR PIR; JN0113; JN0113.
 DR PIR; B25738; B25738.
 DR PIR; JH0172; JH0172.
 DR InterPro; IPR000188; GABA receptor.
 DR InterPro; IPR001175; Neur. channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
 KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 23
 FT CHAIN 24 502
 FT NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT ALPHA-7 CHAIN.
 FT EXTRACELLULAR.
 FT
 FT DOMAIN 24 230
 FT TRANSMEM 231 255
 FT TRANSMEM 262 280
 FT TRANSMEM 296 317
 FT DOMAIN 318 469
 FT TRANSMEM 470 490
 FT DISULFID 150 164
 FT DISULFID 212 213
 FT CARBOHYD 46 46
 FT CARBOHYD 90 90
 FT CARBOHYD 133 133
 FT MUTAGEN 270 270
 FT
 FT CONFLICT 26 27
 FT SEQUENCE 502 AA; 56946 MW; 572325D4309AD2FD CRC64;
 SQ
 Query Match 18.3%; Score 92; DB 1; Length 502;
 Best Local Similarity 100.0%; Pred. No. 1.3e-82;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 275 FMLLVAEIMPATSDSVPLIAQYFASVTMIIVGLSVVTVIVLYQYHHDDPGGKMPKWTWVI 334
 DB 275 FMLLVAEIMPATSDSVPLIAQYFASVTMIIVGLSVVTVIVLYQYHHDDPGGKMPKWTWVI 334
 OY 335 LLNWCWFLRMKRPGEKDVPRACQKQRCSL 366
 DB 335 LLNWCWFLRMKRPGEKDVPRACQKQRCSL 366
 RESULT 3
 ACH7_BOVIN
 ID ACH7_BOVIN STANDARD; PRT; 499 AA.
 AC P54131;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
 GN CHRNA7.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Theria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Adrenal medulla;
 RX MEDLINE=95346009; PubMed=7620615;
 RA Garcia-Guzman M., Sala F., Sala S., Campos-Caro A., Stuehmer W.,
 RA Gutierrez L., Criado M.;

RESULT 5
 ACH7_RAT ACH7_RAT STANDARD; PRT; 502 AA.
 AC Q05941;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
 GN CHRNA7 OR ACRA7.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93147911; PubMed=7678857;
 RA Seguela P., Wadiche J., Dineley-Miller K., Dani J.A., Patrick J.W.,
 RT "Molecular cloning, functional properties, and distribution of rat
 brain alpha 7: a nicotinic cation channel highly permeable to
 calcium.";
 RL J. Neurosci. 13:596-604(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RA Hartley M.;
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 MEMBRANE.
 CC -!- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
 BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
 SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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 DR EMBL; S53987; AAB25224.2; --
 DR EMBL; L31619; AAC33136.1; --
 DR InterPro; IPR000188; GABAA_receptor.
 DR InterPro; IPR001175; Neur channel.
 DR Pfam; PF02911; Neur_chan_1BD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMS; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
 KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 FT SIGNAL 1 22 BY SIMILARITY.
 FT CHAIN 23 502 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT ALPHA-7 CHAIN.
 FT DOMAIN 23 230 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 21 255 POTENTIAL.
 FT TRANSMEM 262 280 POTENTIAL.
 FT TRANSMEM 296 317 POTENTIAL.
 FT DOMAIN 318 469 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 470 490 POTENTIAL.
 FT DISULFID 150 164 BY SIMILARITY.

FT DISULFID 212 213 ASSOCIATED WITH RECEPTOR ACTIVATION
 (BY SIMILARITY).
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 447 447 N -> F (IN REF. 2).
 FT CONFLICT 469 469 P -> R (IN REF. 2).
 SQ SEQUENCE 502 AA; 56410 MW; 00996E74EC7B9A56 CRC64;
 Query Match 12.4%; Score 62; DB 1; Length 502;
 Best Local Similarity 100.0%; Pred. No. 5e-53;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 29 LYKELVKYNYNPLERPVANDSQPLTYVYFSLSLQIMDVDEKQVLTNTIWLQMSWTDHYLQ 88
 DB 29 LYKELVKYNYNPLERPVANDSQPLTYVYFSLSLQIMDVDEKQVLTNTIWLQMSWTDHYLQ 88
 QY 89 WN 90
 DB 89 WN 90
 RESULT 6
 SHT3_HUMAN
 ID SHT3_HUMAN STANDARD; PRT; 478 AA.
 AC P46098;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 5-hydroxytryptamine 3 receptor precursor (5-HT-3) (Serotonin-gated ion
 channel receptor) (5-HT3R).
 GN HTR3A OR HTR3 OR 5HT3R.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hippocampus;
 RX MEDLINE=96018832; PubMed=7565620;
 RA Miyake A., Mochizuki S., Takemoto Y., Akuzawa S.;
 RT "Molecular cloning of human 5-hydroxytryptamine3 receptor:
 heterogeneity in distribution and function among species.";
 RL Mol. Pharmacol. 48:407-416(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Amygdala;
 RX MEDLINE=99127223; PubMed=9928262;
 RA Bruss M., Gothert M., Hayer M., Bonisch H.;
 RT "Molecular cloning of alternatively spliced human 5HT3 receptor
 cDNAs.";
 RL Ann. N.Y. Acad. Sci. 861:234-235(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Publ H.L. III, Ikeda S.R., Aronstam R.S.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR
 AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THIS RECEPTOR IS
 A LIGAND-GATED ION CHANNEL, WHICH WHEN ACTIVATED CAUSES FAST,
 CC DEPOLARIZING RESPONSES IN NEURONS. IT IS A CATION-SPECIFIC, BUT
 CC OTHERWISE RELATIVELY NONSELECTIVE, ION CHANNEL.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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CC EMBL; D49394; BAA08387.1; -.
CC EMBL; AF003079; CAA05852.1; -.
CC EMBL; AF498984; AAM21131.1; -.
CC EMBL; BC002354; AAH02354.1; -.
CC EMBL; HGNC:5297; HTR3A.
CC MIM; 182133; -.
CC InterPro; IPR000188; GABAA_receptor.
CC InterPro; IPR001175; Neur_Channel.
CC Pfam; PF02931; Neur_chan_LBD; 1.
CC Pfam; PF02932; Neur_chan_memb; 1.
CC PRINTS; PR00252; NRIONCHANNEL.
CC TIGRPFMS; TIGR00860; LIC; 1.
CC PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
CC ionic channel; Transmembrane; Receptor; Glycoprotein; Signal;
KW Phosphorylation.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 478 5-HYDROXYTRYPTAMINE 3 RECEPTOR.
FT DOMAIN 24 241 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 242 268 1 (POTENTIAL).
FT DOMAIN 269 273 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 274 292 2 (POTENTIAL).
FT DOMAIN 293 302 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 303 321 3 (POTENTIAL).
FT DOMAIN 322 455 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 456 475 4 (POTENTIAL).
FT DOMAIN 476 478 EXTRACELLULAR (POTENTIAL).
FT DISULFID 157 171 BY SIMILARITY.
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 478 AA; 55280 MW; 24CA9A232286FBC9 CRC64;

Query Match 2.0%; Score 10; DB 1; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.088;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 65 VDEKQVLT 74
    |||||
Db 73 VDEKQVLT 82

RESULT 7
ACH9 HUMAN STANDARD; PRT; 479 AA.
AC Q9UGM1; Q9NVV2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-9 chain precursor.
GN CHR9A9 OR NACHRA9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Embryo;
RA Charpentier E., Partisetti M., Besnard F., Sgard F.;
RT "Cloning and characterization of the human alpha 9 nicotinic
RT acetylcholine receptor."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 7-476 FROM N.A.
RA Nguyen Thuong V., Grando S.A.;
RT "Cloning and characterization of human alpha 9 nicotinic acetylcholine
RT receptor subunit from normal oral epithelial cell."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

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CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE (BY SIMILARITY).
CC -1- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC -----
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EMBL; AJ243342; CAB65091.1; -.
EMBL; AF227732; AAF61920.1; -.
Genew; HGNC:14079; CHR9A9.
MIM; 605116; -.
InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_Channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGRPFMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
Transmembrane; Multigene family.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 479 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
ALPHA-9 CHAIN.
FT DOMAIN 26 237 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 238 262 POTENTIAL.
FT TRANSMEM 269 287 POTENTIAL.
FT TRANSMEM 302 323 POTENTIAL.
FT DOMAIN 324 457 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 458 476 POTENTIAL.
FT DISULFID 155 169 BY SIMILARITY.
FT DISULFID 219 220 ASSOCIATED WITH RECEPTOR ACTIVATION
(BY SIMILARITY).
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 442 442 S -> N (IN REF. 2).
SQ SEQUENCE 479 AA; 54780 MW; 336B46B559C6FF13 CRC64;

Query Match 2.0%; Score 10; DB 1; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.088;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 236 NLLIPCVLIS 245
    |||||
Db 243 NLLIPCVLIS 252

RESULT 8
ACH9 RAT STANDARD; PRT; 479 AA.
AC P43144;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-9 chain precursor.
GN CHR9A9 OR ACHRA9.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Olfactory epithelium;
RX MEDLINE=95042767; PubMed=7954834;
RA Elgoyhen A.B., Johnson D.S., Boulter J., Verter D.E., Heinemann S.F.;


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RT "Alpha 9: an acetylcholine receptor with novel pharmacological
 RL properties expressed in rat cochlear hair cells.";
 CC Cell 79:705-715(1994).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- FUNCTION: IS INVOLVED IN THE CHOLINERGIC EFFERENT INNERVATION OF
 CC COCHLEAR HAIR CELLS AND THUS MAY MODULATE THE ENCODING OF AUDITORY
 CC STIMULI. THIS RECEPTOR POSSESSES BOTH NICOTINIC AND MUSCARINIC
 CC PROPERTIES.
 CC -!- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: DETECTED IN THE NASAL EPITHELIUM, IN THE OUTER
 CC HAIR CELLS OF THE COCHLEA, IN THE PARS TUBERALEM OF THE
 CC HYPOTHALAMUS, AND IN THE DEVELOPING MUSCLE OF THE TONGUE.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC -----
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 CC -----
 CC EMBL; U12336; AAA56720.1; --
 DR InterPro; IPR000188; GABAA receptor.
 DR InterPro; IPR001175; Neur Channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMS; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
 DR Post-synaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 479 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT ALPHA-9 CHAIN.
 FT DOMAIN 26 237 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 238 262 POTENTIAL.
 FT TRANSMEM 269 287 POTENTIAL.
 FT TRANSMEM 302 323 POTENTIAL.
 FT DOMAIN 324 457 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 458 476 POTENTIAL.
 FT DISULFID 155 169 BY SIMILARITY.
 FT DISULFID 219 220 ASSOCIATED WITH RECEPTOR ACTIVATION
 FT (BY SIMILARITY).
 FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 479 AA; 54495 MW; CBAGF45B9DF69287 CRC64;
 Query Match 2.0%; Score 10; DB 1; Length 479;
 Best Local Similarity 100.0%; Pred. No. 0.088;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 236 NLLIPCVLIS 245
 |||||
 Db 243 NLLIPCVLIS 252
 RESULT 9
 SHT3_RAT
 ID SHT3_RAT STANDARD; PRT; 483 AA.
 AC P35563;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 5-hydroxytryptamine 3 receptor precursor (5-HT-3) (Serotonin-gated ion
 GN channel receptor) (5-HT3R).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN NCBF_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Miyake A., Mochizuki S., Akuzawa S., Kon G.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 RN [2].
 CC SEQUENCE OF 22-483 FROM N.A.
 RX MEDLINE=94154206; PubMed=7509203;
 RA Isenberg K.E., Ukun I.A., Holstad S.G., Jafri S., Uchida U.,
 RA Zorumski C.F., Yang J.;
 RT "Partial cDNA cloning and NGF regulation of a rat 5-HT3 receptor
 RT subunit.";
 RL NeuroReport 5:121-124(1993).
 CC -!- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR
 CC 5-HYDROXYTRYPTAMINE (SEROTONIN). A BIOGENIC HORMONE THAT FUNCTION
 CC AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THIS RECEPTOR IS
 CC A LIGAND-GATED ION CHANNEL, WHICH WHEN ACTIVATED CAUSES FAST, BUT
 CC DEPOLARIZING RESPONSES IN NEURONS. IT IS A CATION-SPECIFIC, BUT
 CC OTHERWISE RELATIVELY NONSELECTIVE, ION CHANNEL.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; D49395; BAA08388.1; --
 DR EMBL; U01227; AAA52182.1; --
 DR InterPro; IPR000188; GABAA receptor.
 DR InterPro; IPR001175; Neur Channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMS; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
 DR Ionic channel; Transmembrane; Receptor; Glycoprotein; Signal;
 KW Phosphorylation.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 483 5-HYDROXYTRYPTAMINE 3 RECEPTOR.
 FT DOMAIN 24 246 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 247 273 1 (POTENTIAL).
 FT TRANSMEM 274 278 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 279 297 2 (POTENTIAL).
 FT DOMAIN 298 307 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 308 326 3 (POTENTIAL).
 FT DOMAIN 327 460 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 461 480 4 (POTENTIAL).
 FT DOMAIN 481 483 EXTRACELLULAR (POTENTIAL).
 FT DISULFID 162 176 BY SIMILARITY.
 FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 22 22 E -> K (IN REF. 2).
 FT CONFLICT 306 306 G -> R (IN REF. 2).
 SQ SEQUENCE 483 AA; 55428 MW; ED85257BBCF28A4 CRC64;
 Query Match 2.0%; Score 10; DB 1; Length 483;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 65 VDEKNQVLTT 74
 |||||
 Db 78 VDEKNQVLTT 87
 RESULT 10
 SHT3_MOUSE

ID 5HT3 MOUSE STANDARD; PRT; 487 AA.
AC P23979; Q61225; Q61226;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 5-hydroxytryptamine 3 receptor precursor (5-HT-3) (Serotonin-gated ion channel receptor) (5-HT3R).
GN HTR3A OR HTR3 OR 5HT3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92022603; PubMed=1718042;
RA Maricq A.V., Peterson A.S., Brake A.J., Myers R.M., Julius D.;
RT "Primary structure and functional expression of the 5HT3 receptor, a serotonin-gated ion channel.";
RL Science 254:432-437(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/c; TISSUE=Brain;
RX MEDLINE=94156052; PubMed=8112471;
RA Uetz P., Abdelatty F., Villarroel A., Gundrun R., Weiss B., Koenen M.;
RT "Organisation of the murine 5-HT3 receptor gene and assignment to human chromosome 11.";
RL FEBS Lett. 339:302-306(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=93259238; PubMed=7683998;
RA Hope A.G., Downie D.L., Sutherland L., Lambert J.J., Peters J.A., Burchell B.;
RT "Cloning and functional expression of an apparent splice variant of the murine 5-HT3 receptor A subunit.";
RL Eur. J. Pharmacol. 245:187-192(1993).
RN [4]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC STRAIN=129/Sv;
RX MEDLINE=95157178; PubMed=7854052;
RA Werner P., Kawashima E., Reid J., Hussy N., Lundstrom K., Buell G., Humbert Y., Jones K.A.;
RT "Organization of the mouse 5-HT3 receptor gene and functional expression of two splice variants.";
RL Brain Res. Mol. Brain Res. 26:233-241(1994).
CC -!- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTION AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THIS RECEPTOR IS A LIGAND-GATED ION CHANNEL, WHICH WHEN ACTIVATED CAUSES FAST, DEPOLARIZING RESPONSES IN NEURONS. IT IS A CATION-SPECIFIC, BUT OTHERWISE RELATIVELY NONSELECTIVE, ION CHANNEL.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 5-HT3R-A (SHOWN HERE) AND 5-HT3R-AS; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: BRAIN, SPINAL CORD, AND HEART.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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CC
DR EMBL; M74425; AAA37124.1; -
DR EMBL; Z22772; CAA80453.1; -
DR EMBL; Z22773; CAA80453.1; JOINED.
DR EMBL; X72395; CAA51089.1; -
DR EMBL; X79283; CAA55870.1; -
DR EMBL; X79283; CAA55871.1; -
DR PIR; A40832; A40832.
DR MGD; MGI:96282; Htr3a.

DR InterPro; IPR000188; GABAA receptor.
DR InterPro; IPR001175; Neur Channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NR1ONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR POSITE; PS00236; NEUOTR_ION_CHANNEL; 1.
DR Ionic channel; Transmembrane; Receptor; Glycoprotein; Signal; Phosphorylation; Alternative splicing.
KW SIGNAL 1 23
FT CHAIN 24 487
FT DOMAIN 24 245
FT TRANSMEM 246 272
FT DOMAIN 273 277
FT TRANSMEM 278 296
FT DOMAIN 297 305
FT TRANSMEM 306 324
FT DOMAIN 325 464
FT TRANSMEM 465 484
FT DOMAIN 485 487
FT DISULFID 161 175
FT CARBOHYD 108 108
FT CARBOHYD 174 174
FT CARBOHYD 190 190
FT VARSPIC 383 388
FT CONFLICT 31 31
FT CONFLICT 74 74
FT CONFLICT 302 302
FT CONFLICT 384 384
FT CONFLICT 393 393
SQ SEQUENCE 487 AA; 56056 MW; D0148867C8536D66 CRC64;
Query Match 2.0%; Score 10; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 65 VDEKNQVLTT 74
DB 77 VDEKNQVLTT 86
RESULT 11
ACHX ONCVO STANDARD; PRT; 436 AA.
AC P54247;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acetylcholine receptor protein, non-alpha chain (Fragment).
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Filarioidea; Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94299155; PubMed=8026747;
RA Ajun P.M., Egwang T.G.;
RT "Cloning of a cDNA encoding a putative nicotinic acetylcholine receptor subunit of the human filarial parasite Onchocerca volvulus.";
RL Gene 144:127-129(1994).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA MEMBRANE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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CC EMBL; L20465; AAA21823.1; -
CC EMBL; L12543; AAA29415.1; -
CC InterPro; IPR001188; GABAA receptor.
CC InterPro; IPR001175; Neur Channel.
CC Pfam; PF02931; Neur_chan_LBD; 1.
CC Pfam; PF02932; Neur_chan_memb; 1.
CC PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
KW Multigene family.
FT NON_TER 1 1 EXTRACELLULAR (POTENTIAL).
FT DOMAIN <1 195 POTENTIAL.
FT TRANSMEM 196 219 POTENTIAL.
FT TRANSMEM 227 245 POTENTIAL.
FT TRANSMEM 261 280 POTENTIAL.
FT DOMAIN 281 404 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 405 423 POTENTIAL.
FT DISULFID 89 103 BY SIMILARITY.
FT CARBOHYD 52 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 436 AA; 51340 MW; 58051BFE59A4555F CRC64;

Query Match 1.8%; Score 9; DB 1; Length 436;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 IDVRWPFED 160
DB 91 IDVRWPFED 99

RESULT 12
ACHX HUMAN
ID ACHX HUMAN STANDARD; PRT; 450 AA.
AC Q9GZ6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-10 chain precursor
DE (Nicotinic acetylcholine receptor subunit alpha 10) (NACHR alpha 10).
DE CHRNA10 OR NACHRA10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Sgard F., Charpentier E., Bertrand S., Walker N., Agnel M., Graham D.,
RA Caput D., Bertrand D., Besnard F.;
RT "Cloning and expression of a novel nicotinic alpha10 subunit from
RT human that confers functionality to the alpha9 subunit.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Inner ear, and Tonsil;
RX MEDLINE=21248672; PubMed=11350119;
RA Lustig L.R., Peng H., Hiel H., Yamamoto T., Fuchs P.A.;
RT "Molecular cloning and mapping of the human nicotinic acetylcholine
RT receptor alpha10 (CHRNA10).";
RL Genomics 73:272-283 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RA Vandenberk I., van der Helm L., Nieuwstraten D.M., Verfaillie C.,
RA Kremer A., van der Spek P., Masure S., Hofnagel E., Yon J.,
RA Groot Kormelink P.J., Luyten W.H., Grantham C.J.;
RT "Identification and functional characterisation of a novel human
RT neuronal nicotinic acetylcholine receptor subunit alpha 10.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
MEMBRANE.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Expressed in inner-ear tissue, tonsil,
immortalized B-cells, cultured T-cells and peripheral blood
lymphocytes.
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

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CC EMBL; AJ278118; CAC20435.1; -
CC EMBL; AF199235; AAG00795.2; -
CC EMBL; AF327367; AAK14333.1; -
CC EMBL; AJ295237; CAC16144.1; -
CC Genew; HGNC:13800; CHRNA10.
CC MIM; 606372; -
CC InterPro; IPR001188; GABAA receptor.
CC InterPro; IPR001175; Neur Channel.
CC Pfam; PF02931; Neur_chan_LBD; 1.
CC Pfam; PF02932; Neur_chan_memb; 1.
CC PRINTS; PR00252; NRIONCHANNEL.
CC TIGRFAMs; TIGR00860; LIC; 1.
CC PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 450 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
ALPHA-10 CHAIN.
FT DOMAIN 25 237 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 238 258 POTENTIAL.
FT TRANSMEM 268 288 POTENTIAL.
FT TRANSMEM 302 322 POTENTIAL.
FT DOMAIN 323 428 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 429 449 POTENTIAL.
FT DISULFID 154 168 BY SIMILARITY.
FT DISULFID 218 219 ASSOCIATED WITH RECEPTOR ACTIVATION
(BY SIMILARITY).
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 450 AA; 49704 MW; 0A1DAD32D9069870 CRC64;

Query Match 1.8%; Score 9; DB 1; Length 450;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 EPPYDVTFT 223
DB 221 EPPYDVTFT 229

RESULT 13
ACHI CAEL
ID ACHI CAEL STANDARD; PRT; 498 AA.
AC P48180;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acetylcholine receptor like protein, alpha-type chain precursor.
GN F25G6.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=96196478; PubMed=8627624;

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RA Ballivet M., Alliod C., Bertrand S., Bertrand D.;
RT "Nicotinic acetylcholine receptors in the nematode Caenorhabditis
RL elegans.";
RN J. Mol. Biol. 258:261-269(1996).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Nelson J., Wohldmann P.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: POSSIBLE ACETYLCHOLINE RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC
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CC
DR EMBL; X83887; CAA58764.1; -
DR EMBL; AF022973; AAC25796.1; -
DR HSP; F58154; I19B.
DR WormPep; F25G6.3; CE09639.
DR InterPro; IPR001188; GABAA_receptor.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
KW Transmembrane; Signal.
FT SIGNAL 1 19
FT CHAIN 20 498
FT DOMAIN 20 230 ACETYLCHOLINE RECEPTOR LIKE PROTEIN,
FT TRANSMEM 231 252 ALPHA-TYPE CHAIN.
FT TRANSMEM 261 279 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 295 314 POTENTIAL.
FT DOMAIN 315 472 POTENTIAL.
FT TRANSMEM 473 493 CYTOPLASMIC (POTENTIAL).
FT DISULFID 147 161 POTENTIAL.
FT DISULFID 211 212 BY SIMILARITY.
FT CARBOHYD 43 43 ASSOCIATED WITH RECEPTOR ACTIVATION
FT CARBOHYD 93 93 (BY SIMILARITY).
FT CARBOHYD 93 93 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 498 AA; 57169 MW; E463ABB40AC9FA82 CRC64;

Query Match 1.8%; Score 9; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 MRRRLYYG 234
DB 225 MRRRLYYG 233

RESULT 14
ACH5 CAEEL STANDARD; PRT; 511 AA.
AC Q23022; Q17408; P91265; O02559;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acetylcholine receptor, alpha-type subunit unc-38 precursor.
GN UNC-38 OR F21F3.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=97368239; PubMed=9221782;
RA Fleming J.T., Squire M.D., Barnes T.M., Tornoe C., Matsuda K.,
RA Ahnn J., Fire A., Sulston J.E., Barnard E.A., Sattelle D.B.,
RA Lewis J.A.;
RT "Caenorhabditis elegans levamisole resistance genes lev-1, unc-29,
RT and unc-38 encode functional nicotinic acetylcholine receptor
RT subunits.";
RL J. Neurosci. 17:5843-5857(1997).
[2]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Geisel C., Kramer J., Elliott G.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
[3]
RN
RP REVISIONS.
RA Waterston R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ACETYLCHOLINE RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC
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CC
DR EMBL; X98600; CAA67197.1; -
DR EMBL; X98599; CAA67196.1; -
DR EMBL; U88175; AAB42282.2; -
DR WormPep; F21F3.5; CE09535.
DR InterPro; IPR001188; GABAA_receptor.
DR InterPro; IPR001175; Neur Channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
KW Transmembrane; Signal.
FT SIGNAL 1 16
FT CHAIN 17 511
FT DOMAIN 17 261 ACETYLCHOLINE RECEPTOR, ALPHA-TYPE
FT TRANSMEM 262 282 SUBUNIT UNC-38.
FT TRANSMEM 291 311 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 324 344 POTENTIAL.
FT TRANSMEM 345 464 POTENTIAL.
FT TRANSMEM 465 485 CYTOPLASMIC (POTENTIAL).
FT DISULFID 151 165 BY SIMILARITY.
FT DISULFID 238 239 BY SIMILARITY.
FT CARBOHYD 124 124 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 511 AA; 59454 MW; 19F690731B23E1A6 CRC64;

Query Match 1.8%; Score 9; DB 1; Length 511;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 IDVRWFFPD 160
DB 153 IDVRWFFPD 161

RESULT 15
ACH1 SCHGR STANDARD; PRT; 557 AA.
ID ACH1 SCHGR
AC P23414;
DT 01-NOV-1991 (Rel. 20, Created)

```

DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acetylcholine receptor protein, alpha-L1 chain precursor.
OS Schistocerca gregaria (Desert locust).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC Acridomorpha; Acridoidea; Acrididae; Cyrtacanthacridinae;
OC Schistocerca.
OX NCBI_TaxID=7010;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91092263; PubMed=1702381;
RA Marshall J., Buckingham S.D., Shingai R., Lunt G.G., Goosey M.W.,
RA Darlison M.G., Sattelle D.B., Barnard E.A.;
RT "Sequence and functional expression of a single alpha subunit of an
RT insect nicotinic acetylcholine receptor.";
RL EMBO J. 9:4391-4398(1990).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC -----
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CC -----
DR EMBL; X55439; CAA39081.1; -.
DR PIR; S12359; S12359.
DR InterPro; IPR000188; GABAA receptor.
DR InterPro; IPR001175; Neur_chan.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PRO0252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 557 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-L1
FT CHAIN EXTRACELLULAR.
FT DOMAIN 24 244
FT TRANSMEM 245 266
FT TRANSMEM 274 294
FT TRANSMEM 308 329
FT DOMAIN 330 500
FT TRANSMEM 501 523
FT DISULFID 151 165
FT DISULFID 224 225
FT CARBOHYD 47 47
FT CARBOHYD 235 235
FT DOMAIN 382 400
FT DOMAIN 406 422
FT SEQUENCE 557 AA; 63026 MW; 168389C87DFDF3E CRC64;
Query Match 1.8%; Score 9; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 254 LPADSGEKI 262
Db 266 LPADSGEKI 274

Search completed: June 20, 2003, 19:12:10
Job time : 28 secs

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OM protein - protein search, using sw model

Run on: June 20, 2003, 19:09:27 ; Search time 43 Seconds
(without alignments)
1122.313 Million cell updates/sec

Title: US-09-954-936-2
Perfect score: 502
Sequence: 1 MRCSPGGVWLAAASLLHVS.....TIGILSGAPNFEAVSKDFA 502

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 6

Total number of hits satisfying chosen parameters: 2355

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	289	57.6	502	1 ACHUA7	nicotinic acetylch
2	267	53.2	502	2 GQ2259	alpha 7 neuronal n
3	92	18.3	502	2 JN0113	nicotinic acetylch
4	62	12.4	502	2 T01378	nicotinic receptor
5	62	12.4	502	2 A57175	nicotinic acetylch
6	27	5.4	511	2 JH0173	alpha-bungarotoxin
7	12	2.4	565	2 T23843	hypothetical prote
8	11	2.2	456	2 T24504	hypothetical prote
9	10	2.0	462	2 I58179	5HT3 receptor subu
10	10	2.0	479	2 A55382	nicotinic acetylch
11	10	2.0	489	2 S41757	5-hydroxytryptamin
12	10	2.0	542	2 T19862	hypothetical prote
13	9	1.8	336	2 T16652	hypothetical prote
14	9	1.8	466	2 PC4296	nicotinic acetylch
15	9	1.8	498	2 S68598	nicotinic acetylch
16	9	1.8	511	2 T43634	nicotinic acetylch
17	9	1.8	534	2 T25720	hypothetical prote
18	9	1.8	557	2 S12359	nicotinic acetylch
19	9	1.8	576	1 ACPFA2	nicotinic acetylch
20	8	1.6	133	2 S56647	trypsin inhibitor
21	8	1.6	133	2 S56648	trypsin inhibitor
22	8	1.6	141	2 A40463	integrin alpha-6 c
23	8	1.6	149	2 B40463	integrin alpha-6 c
24	8	1.6	245	2 C64616	hypothetical prote
25	8	1.6	356	2 D86382	hypothetical prote
26	8	1.6	416	1 ACCH3N	nicotinic acetylch
27	8	1.6	452	2 D83609	probable glutamine
28	8	1.6	461	2 T25671	hypothetical prote
29	8	1.6	513	1 ACCHD1	nicotinic acetylch

30	8	1.6	517	2 A60916	nicotinic acetylch
31	8	1.6	521	2 C28529	nicotinic acetylch
32	8	1.6	559	2 E89134	protein F25G6.4 [i
33	8	1.6	560	2 T19622	hypothetical prote
34	8	1.6	567	1 ACPFA1	nicotinic acetylch
35	8	1.6	1072	2 A38457	integrin alpha-6 c
36	7	1.4	68	2 G69093	histone HmtA2 - Me
37	7	1.4	69	2 A35959	archaeal histone H
38	7	1.4	101	2 E75487	v-type ATP synthas
39	7	1.4	116	2 T05366	auxin-induced prot
40	7	1.4	127	2 B97810	hypothetical prote
41	7	1.4	128	2 S70623	cytochrome P450 CY
42	7	1.4	130	2 G25733	T-cell receptor al
43	7	1.4	130	2 E87384	cytochrome c famil
44	7	1.4	143	2 E86824	hypothetical prote
45	7	1.4	144	2 S01898	psbB protein - Esc

ALIGNMENTS

RESULT 1

ACHUA7

nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - human
N:Alternate names: cholinergic nicotinate receptor alpha-7 chain
C:Species: Homo sapiens (man)

C>Date: 12-Aug-1996 #sequence revision 31-Jan-1997 #text_change 22-Jun-1999

C:Accession: I37185; A54194; S60309

R: Peng, X.; Katz, M.; Gerzanich, V.; Anand, R.; Lindstrom, J.

Mol. Pharmacol. 45, 546-554, 1994

A: Title: Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from the omers expressed in Xenopus oocytes.

A: Reference number: I37185; MUID: 94195283; PMID: 8145738

A: Accession: I37185

A: Status: translated from GB/EMBL/DDBJ

A: Molecule type: mRNA

A: Residues: 1-502 <PEN>

A: Cross-references: EMBL:X70297; NID:G496606; PIDN:CAA49778.1; PID:G496607

A: Experimental source: Brain neuroblastoma cell line SHSY-5Y

R: Chini, B.; Raimond, E.; Elgoyhen, A.B.; Moralli, D.; Balzaretti, M.; Heinemann, S.

Genomics 19, 379-381, 1994

A: Title: Molecular cloning and chromosomal localization of the human alpha-7-nicotinic A: Reference number: A54194; MUID: 94245214; PMID: 8188270

A: Accession: A54194

A: Molecule type: mRNA

A: Residues: 24-363, 'S', 365-374, 'A', 376-408, 'AWPAP', 414-502 <CHI>

A: Cross-references: GB:Z23141; NID:G457736; PIDN:CAA80672.1; PID:G457737

A: Experimental source: retina

C: Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is localized

C: Genetics:

A: Gene: GDB:CHRNA7

A: Cross-references: GDB:138751; OMIM:118511

A: Map position: 15q14-15q14

A: Note: defects in this gene have been associated with mental retardation and schizophrenia

C: Superfamily: acetylcholine receptor

C: Keywords: brain; glycoprotein; heteropentamer; ion channel; neurotransmitter receptor

F: 1-23/Domain: signal sequence #status predicted <SIG>

F: 24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pred

F: 231-254/Domain: transmembrane #status predicted <TR1>

F: 262-280/Domain: transmembrane #status predicted <TR2>

F: 296-317/Domain: transmembrane #status predicted <TR3>

F: 470-488/Domain: transmembrane #status predicted <TR4>

F: 46,90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted

F: 150-164/Bifulfide bonds: #status predicted

F: 365,413/Binding site: phosphate (Ser) (covalent) #status predicted

F: 415/Binding site: phosphate (Thr) (covalent) #status predicted

F: 442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 57.6%; Score 289; DB 1; Length 502;

Best Local Similarity 99.6%; Pred. No. 3.3e-281;

Matches 489; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 LAASLLHVSLOGBFQKLYKELVKNYNPLRPVANDSQPLTVTVFSLQLQIMDVDEKNQV 71
 Db 12 LAASLLHVSLOGBFQKLYKELVKNYNPLRPVANDSQPLTVTVFSLQLQIMDVDEKNQV 71
 QY 72 LTTNIWLQSWTDHYLQWNVSEYPGVKTVPDGOIWKPDILLYNLSADERFDFATFHTNVL 131
 Db 72 LTTNIWLQSWTDHYLQWNVSEYPGVKTVPDGOIWKPDILLYNLSADERFDFATFHTNVL 131
 QY 132 VNSSGHCQYLPPGIFKSSCYIDVRWFPDVOHCKLKFGWSYGSWGLDLQWQOEADISGYI 191
 Db 132 VNSSGHCQYLPPGIFKSSCYIDVRWFPDVOHCKLKFGWSYGSWGLDLQWQOEADISGYI 191
 QY 192 PNGEWDLVGIPIGRKSERFECCKEPEYDPDVTFTVMRRRTLYYGLNLLIPCVLISALALLV 251
 Db 192 PNGEWDLVGIPIGRKSERFECCKEPEYDPDVTFTVMRRRTLYYGLNLLIPCVLISALALLV 251
 QY 252 FILPADSGEKISLIGITVLLSLTFVMLLVAEIMPATSDSVPLIAQYFASFTMIIVGLSVVVT 311
 Db 252 FILPADSGEKISLIGITVLLSLTFVMLLVAEIMPATSDSVPLIAQYFASFTMIIVGLSVVVT 311
 QY 312 VIVLQVHHDDPGGKMPKTRVILLNWCAMFLMRKRPGEKVRPACQHKORRCSLASVEM 371
 Db 312 VIVLQVHHDDPGGKMPKTRVILLNWCAMFLMRKRPGEKVRPACQHKORRCSLASVEM 371
 QY 372 SAVAPPASNGNLLYIGFRGLDGVHCVPTDPSGVVCGRMACSPTHDEHLLHGGQPPGDP 431
 Db 372 SAVAPPASNGNLLYIGFRGLDGVHCVPTDPSGVVCGRMACSPTHDEHLLHGGQPPGDP 431
 QY 432 DLAKILEEVYIANRFRQDESEAVCEWKFACVDRCLCLMAPSVFTIICITIGILMSAP 491
 Db 432 DLAKILEEVYIANRFRQDESEAVCEWKFACVDRCLCLMAPSVFTIICITIGILMSAP 491
 QY 492 NFVEAVSKDFA 502
 Db 492 NFVEAVSKDFA 502

RESULT 2

G02259
 alpha 7 neuronal nicotinic acetylcholine receptor - human
 C:Species: Homo sapiens (man)
 C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999
 C:Accession: G02259
 R:Leonard, S.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: H00936
 A:Accession: G02259
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-502 <LEO>
 A:Cross-references: EMBL:U40583; NID:g1125076; PIDN:AAA83561.1; PID:g1125077
 C:Superfamily: acetylcholine receptor

Query Match 53.2%; Score 267; DB 2; Length 502;
 Best Local Similarity 99.7%; Pred. No. 3.7e-259;
 Matches 367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 135 SGHCQYLPPGIFKSSCYIDVRWFPDVOHCKLKFGWSYGSWGLDLQWQOEADISGYIPNG 194
 Db 135 SGHCQYLPPGIFKSSCYIDVRWFPDVOHCKLKFGWSYGSWGLDLQWQOEADISGYIPNG 194
 QY 195 EMDLVGIPGRKSERFECCKEPEYDPDVTFTVMRRRTLYYGLNLLIPCVLISALALLVFL 254
 Db 195 EMDLVGIPGRKSERFECCKEPEYDPDVTFTVMRRRTLYYGLNLLIPCVLISALALLVFL 254
 QY 255 PADSGEKISLIGITVLLSLTFVMLLVAEIMPATSDSVPLIAQYFASFTMIIVGLSVVVTIV 314
 Db 255 PADSGEKISLIGITVLLSLTFVMLLVAEIMPATSDSVPLIAQYFASFTMIIVGLSVVVTIV 314
 QY 315 LOYHHDDPGGKMPKTRVILLNWCAMFLMRKRPGEKVRPACQHKORRCSLASVEMSAV 374
 Db 315 LOYHHDDPGGKMPKTRVILLNWCAMFLMRKRPGEKVRPACQHKORRCSLASVEMSAV 374

QY 375 APPASNGNLLYIGFRGLDGVHCVPTDPSGVVCGRMACSPTHDEHLLHGGQPPGDDPLA 434
 Db 375 APPASNGNLLYIGFRGLDGVHCVPTDPSGVVCGRMACSPTHDEHLLHGGQPPGDDPLA 434
 QY 435 KILBEVYIANRFRQDESEAVCEWKFACVDRCLCLMAPSVFTIICITIGILMSAPNFV 494
 Db 435 KILBEVYIANRFRQDESEAVCEWKFACVDRCLCLMAPSVFTIICITIGILMSAPNFV 494
 QY 495 EAVSKDFA 502
 Db 495 EAVSKDFA 502

RESULT 3

JN0113
 nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - chicken
 N:Alternate names: alpha-bungarotoxin-binding protein alpha chain
 C:Species: Gallus gallus (chicken)
 C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Aug-1999
 C:Accession: JN0113; JH0172; S28018; B25738; S26566
 R:Couturier, S.; Bertrand, D.; Matter, J.M.; Hernandez, M.C.; Bertrand, S.; Millar, N.; Neuron 5, 847-856, 1990
 A:Title: A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is developmental
 A:Reference number: JN0113; MUID:91097796; PMID:1702646
 A:Accession: JN0113
 A:Molecule type: DNA
 A:Residues: 1-502 <COU>
 A:Cross-references: GB:X68586; NID:g287756; PIDN:CAA48576.1; PID:g287757
 A:Experimental source: white leghorn; brain
 R:Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.
 Neuron 5, 35-48, 1990
 A:Title: Brain alpha-bungarotoxin binding protein cDNAs and MAb reveal subtypes of thi
 A:Reference number: JH0172; MUID:90315158; PMID:2369519
 A:Accession: JH0172
 A:Molecule type: mRNA
 A:Residues: 1-502 <SCH>
 A:Cross-references: EMBL:X52295; NID:g63077; PIDN:CAA36543.1; PID:g63078
 A:Experimental source: brain
 R:Matter-Sadzinski, L.; Hernandez, M.C.; Roztocil, T.; Ballivet, M.; Matter, J.M.
 EMBO J. 11, 4529-4538, 1992
 A:Title: Neuronal specificity of the alpha7 nicotinic acetylcholine receptor promoter d
 A:Reference number: S28018; MUID:93049204; PMID:1425587
 A:Accession: S28018
 A:Molecule type: DNA
 A:Residues: 1-18 <MAS>
 A:Cross-references: EMBL:X68246; GB:S49751; NID:g65319; PIDN:CAA48317.1; PID:g65320
 A:Experimental source: white leghorn; erythrocyte
 R:Conti-Tronconi, B.M.; Dunn, S.M.J.; Barnard, E.A.; Dolly, J.O.; Lai, F.A.; Ray, N.; R
 Proc. Natl. Acad. Sci. U.S.A. 82, 5208-5212, 1985
 A:Title: Brain and muscle nicotinic acetylcholine receptors are different but homologou
 A:Reference number: A94055; MUID:85270494; PMID:3860855
 A:Accession: B25738
 A:Molecule type: protein
 A:Residues: 24-25, 'ET', 28-41, 'X', 43-45, 'X', 47 <CON>
 C:Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is localized

C:Genetics:
 A:Introns: 19/1; 65/3; 80/3; 117/2; 144/1; 200/1; 265/1; 294/1; 330/3
 C:Superfamily: acetylcholine receptor
 C:Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprotein
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pred
 F:231-254/Domain: transmembrane #status predicted <TR1>
 F:262-280/Domain: transmembrane #status predicted <TR2>
 F:296-317/Domain: transmembrane #status predicted <TR3>
 F:470-488/Domain: transmembrane #status predicted <TR4>
 F:46, 90, 133/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:365, 367, 413, 427, 465/Binding site: phosphate (Ser) (covalent) #status predicted
 F:415/Binding site: phosphate (Thr) (covalent) #status predicted
 F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 18.3%; Score 92; DB 2; Length 502;
 Best Local Similarity 100.0%; Pred. No. 1.1e-83;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 275 FMLLVAEIMPATSDVPLIAQYFASFTMLIIVGLSVVVTVIVLOYHHHDPDGGKMPKWTTRVI 334
 |||||
 Db 275 FMLLVAEIMPATSDVPLIAQYFASFTMLIIVGLSVVVTVIVLOYHHHDPDGGKMPKWTTRVI 334
 |||||
 Qy 335 LLNWCWFLRMKRGEDKVRPACQKORRCSL 366
 |||||
 Db 335 LLNWCWFLRMKRGEDKVRPACQKORRCSL 366
 |||||

RESULT 4

T01378
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000
 C:Accession: T01378
 R;Seguela, P.; Wadiche, J.; Dineley-Miller, K.; Dani, J.A.; Patrick, J.W.
 J. Neurosci. 13, 596-604, 1993
 A:Title: Molecular cloning, functional properties, and distribution of rat brain alpha 7
 A:Reference number: Z14310; MUID:93147931; PMID:7678857
 A:Accession: T01378
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-502 <SEG>
 A:Cross-references: EMBL:S53987; NID:G264770; PIDN:AAB25224.2; PID:G5705903
 A:Experimental source: brain
 C:Superfamily: acetylcholine receptor

Query Match 12.4%; Score 62; DB 2; Length 502;
 Best Local Similarity 100.0%; Pred. No. 1.3e-53;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 LYKELVKNYNPLERPANDSOPLTIVYFSLSLQIMDVDEKKNQVLTNNIWLQMSWTDHYLQ 88
 |||||
 Db 29 LYKELVKNYNPLERPANDSOPLTIVYFSLSLQIMDVDEKKNQVLTNNIWLQMSWTDHYLQ 88
 |||||

Qy 89 WN 90
 ||
 Db 89 WN 90
 ||

RESULT 5

A57175
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 20-Aug-1999
 C:Accession: A57175
 R;Orr-Urtreger, A.; Seldin, M.F.; Baldini, A.; Beaudet, A.L.
 Genomics 26, 399-402, 1995
 A:Title: Cloning and mapping of the mouse alpha7-neuronal nicotinic acetylcholine receptor
 A:Reference number: A57175; MUID:95324936; PMID:7601470
 A:Accession: A57175
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-502 <ORR>
 A:Cross-references: GB:I37663; NID:G790853; PIDN:AAC42053.1; PID:G790854
 A:Superfamily: acetylcholine receptor

C:Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprotein;
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status predicted
 F:231-254/Domain: transmembrane #status predicted <TR1>
 F:262-280/Domain: transmembrane #status predicted <TR2>
 F:296-317/Domain: transmembrane #status predicted <TR3>
 F:470-488/Domain: transmembrane #status predicted <TR4>
 F:46,90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:365,413,427/Binding site: phosphate (Ser) (covalent) #status predicted
 F:415/Binding site: phosphate (Thr) (covalent) #status predicted
 F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 12.4%; Score 62; DB 2; Length 502;
 Best Local Similarity 100.0%; Pred. No. 1.3e-53;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 LYKELVKNYNPLERPANDSOPLTIVYFSLSLQIMDVDEKKNQVLTNNIWLQMSWTDHYLQ 88
 |||||
 Db 29 LYKELVKNYNPLERPANDSOPLTIVYFSLSLQIMDVDEKKNQVLTNNIWLQMSWTDHYLQ 88
 |||||
 Qy 89 WN 90
 ||
 Db 89 WN 90
 ||

RESULT 6

JH0173
 C:Species: Gallus gallus (chicken)
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Aug-1999
 C:Accession: JH0173
 R;Schoeffer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.
 Neuron 5, 35-48, 1990
 A:Title: Brain alpha-bungarotoxin binding protein cDNAs and MBs reveal subtypes of thi

A:Reference number: JH0172; MUID:90315158; PMID:2369519
 A:Accession: JH0173
 A:Molecule type: mRNA
 A:Residues: 1-511 <SCH>
 A:Cross-references: GB:X52296; NID:G63081; PIDN:CAA36544.1; PID:G63082
 A:Experimental source: brain
 A:Note: this sequence is similar to acetylcholine receptor alpha chains
 C:Comment: Alpha-bungarotoxin binding proteins are localized to extrasynaptic pseudodend
 C:Superfamily: acetylcholine receptor
 C:Keywords: glycoprotein; transmembrane protein
 F:1-30/Domain: signal sequence #status predicted <SIG>
 F:31-510/Product: alpha-bungarotoxin binding protein alpha-2 chain #status predicted <A
 F:239-282/Domain: transmembrane #status predicted <TM1>
 F:270-288/Domain: transmembrane #status predicted <TM2>
 F:304-323/Domain: transmembrane #status predicted <TM3>
 F:479-496/Domain: transmembrane #status predicted <TM4>
 F:54/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 5.4%; Score 27; DB 2; Length 511;
 Best Local Similarity 100.0%; Pred. No. 1.6e-18;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 247 LALLVFLLPADSGEKISIGITVLLSLT 273
 |||||
 Db 255 LALLVFLLPADSGEKISIGITVLLSLT 281
 |||||

RESULT 7

T23843
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T23843
 R;Coles, L.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: Z19807
 A:Accession: T23843
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-565 <WIL>
 A:Cross-references: EMBL:Z68118; PIDN:CAA92184.1; GSPDB:GN00028; CESP:R01E6.4
 A:Experimental source: clone R01E6
 C:Genetics:

A:Map position: X
 A:Gene: CESP:R01E6.4
 A:Introns: 43/3; 84/3; 121/2; 155/3; 190/1; 253/2; 300/3; 364/2; 398/3; 444/3; 500/3

C:Superfamily: acetylcholine receptor

Query Match 2.4%; Score 12; DB 2; Length 565;
 Best Local Similarity 100.0%; Pred. No. 0.0019;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 64 DVDEKKNQVLTNN 75
 |||||
 Db 68 DVDEKKNQVLTNN 79
 |||||

RESULT 8

T24504
Hypothetical protein T05C12.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T24504
R:Burton, J.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z19901
A:Accession: T24504
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-456 <WIL>
A:Cross-references: EMBL:Z66500; PIDN:CAA911304.1; GSPDB:GN00020; CBSP:T05C12.2
A:Experimental source: clone T05C12
C:Genetics:
A:Gene: CBSP:T05C12.2
A:Map position: 2
A:Introns: 30/3; 75/3; 99/1; 117/2; 151/3; 189/1; 249/1; 314/3; 379/1; 416/3
C:Superfamily: acetylcholine receptor

Query Match 2.2%; Score 11; DB 2; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 QIMDVDEKNQV 71

|||||

Db 56 QIMDVDEKNQV 66

RESULT 9

I58179
5HT3 receptor subunit - rat (fragment)
C:Species: Rattus sp. (rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C:Accession: I58179
R:Isenberg, K.E.; Ukhun, I.A.; Holstad, S.G.; Jafri, S.; Uchida, U.; Zorumski, C.F.; Yan
Neuroreport 5, 121-124, 1993
A:Title: Partial cDNA cloning and NGF regulation of a rat 5-HT3 receptor subunit.
A:Reference number: I58179; MUID:94154206; PMID:7509203
A:Accession: I58179
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-462 <RES>
A:Cross-references: EMBL:U01227; NID:G402245; PIDN:AAA52182.1; PID:G402246
C:Superfamily: acetylcholine receptor

Query Match 2.0%; Score 10; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 VDEKNQVLTT 74

|||||

Db 57 VDEKNQVLTT 66

RESULT 10

A55382
nicotinic acetylcholine receptor alpha-9 chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 20-Aug-1999
C:Accession: A55382
R:Elgoyhen, A.B.; Johnson, D.S.; Boulter, J.; Vetter, D.E.; Heinemann, S.
Cell 79, 705-715, 1994
A:Title: alpha9: an acetylcholine receptor with novel pharmacological properties expressed in *Xenopus* oocytes
A:Reference number: A55382; MUID:95042767; PMID:7954834
A:Accession: A55382
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-479 <ELG>
A:Cross-references: GB:U12336; NID:G595480; PIDN:AAA56720.1; PID:G595481

C:Superfamily: acetylcholine receptor
C:Keywords: neurotransmitter receptor

Query Match 2.0%; Score 10; DB 2; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 NLLIPCVLIS 245

|||||

Db 243 NLLIPCVLIS 252

RESULT 11

S41757
5-hydroxytryptamine-3 receptor - mouse
N:Alternate names: serotonin-gated ion channel 5HT3
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 05-Nov-1999
C:Accession: S41757; S43205; S48111; S45019; S40832; I48229; I48230
R:Uetz, P.; Abdelatty, F.; Villarroel, A.; Rappold, G.; Weiss, B.; Koenen, M.
FEBS Lett. 339, 302-306, 1994
A:Title: Organisation of the murine 5-HT(3) receptor gene and assignment to human chromosome 14
A:Reference number: S41757; MUID:94156052; PMID:8112471
A:Accession: S41757
A:Molecule type: DNA
A:Residues: 1-489 <UET1>
A:Cross-references: EMBL:Z22772
A:Note: the authors translated the codon TAC for residue 142 as His, GTG for residue 144
R:Uetz, P.
submitted to the EMBL Data Library, May 1993
A:Reference number: S43205
A:Accession: S43205
A:Molecule type: DNA
A:Residues: 1-30, 'E', 33-303, 305-311, 'I', 313-385, 'T', 387-489 <UET2>
A:Cross-references: EMBL:Z22772
R:Hope, A.G.; Downie, D.L.; Sutherland, L.; Lambert, J.J.; Peters, J.A.; Burchell, B.
Eur. J. Pharmacol. 245, 187-192, 1993
A:Title: Cloning and functional expression of an apparent splice variant of the murine 5-HT3 receptor
A:Reference number: S48111; MUID:93259238; PMID:7683998
A:Accession: S48111
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-74, 'V', 76-384, 391-489 <HOP>
A:Cross-references: EMBL:X72395; NID:G313863; PIDN:CAA51089.1; PID:G313864
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1993
R:Werner, P.; Kawashima, E.; Reid, J.; Hussy, N.; Lundström, K.; Buell, G.; Humbert, Y.
submitted to the EMBL Data Library, May 1994
A:Description: Organization of the mouse 5HT3 receptor gene and functional expression in *Xenopus* oocytes
A:Reference number: S45019
A:Accession: S45019
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-394, 'T', 396-489 <WER>
A:Cross-references: EMBL:X79283; NID:G488693; PIDN:CAA55871.1; PID:G488694
A:Accession: S45020
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-384, 391-394, 'T', 396-489 <WE2>
A:Cross-references: EMBL:X79283; NID:G488693; PIDN:CAA55871.1; PID:G488695
R:Maricq, A.V.; Peterson, A.S.; Brake, A.J.; Myers, R.M.; Julius, D.
Science 254, 432-437, 1991
A:Title: Primary structure and functional expression of the 5HT-3 receptor, a serotonin-gated ion channel
A:Reference number: A40832; MUID:92022603; PMID:1718042
A:Accession: A40832
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-7, 'G', 8-30, 'E', 33-303, 305-489 <MAR>
A:Cross-references: GB:M74425
R:Werner, P.; Kawashima, E.; Reid, J.; Hussy, N.; Lundström, K.; Buell, G.; Humbert, Y.
Brain Res. Mol. Brain Res. 26, 233-241, 1994
A:Title: Organization of the mouse 5-HT3 receptor gene and functional expression of two variants
A:Reference number: I48229; MUID:95157178; PMID:7854052
A:Accession: I48229

A;Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A;Residues: 1-384,391-394,T',396-489 <RES>
A;Cross-references: EMBL:X9283; NID:g488693; PIDN:CAA55871.1; PID:g488695
A;Accession: I48230
A;Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A;Residues: 1-394,T',396-489 <RE2>
A;Cross-references: EMBL:X9283; NID:g488693; PIDN:CAA55870.1; PID:g488694
C;Genetics:
A;Intons: 23/1; 78/3; 93/3; 130/2; 187/1; 240/3; 311/1; 385/1
C;Superfamily: acetylcholine receptor
C;Keywords: alternative splicing; ion channel; neurotransmitter receptor; transmembrane
F;247-273/Domain: transmembrane #status predicted <TM1>
F;279-297/Domain: transmembrane #status predicted <TM2>
F;308-326/Domain: transmembrane #status predicted <TM3>
F;467-486/Domain: transmembrane #status predicted <TM4>

Query Match 2.0%; Score 10; DB 2; Length 489;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 VDEKNQVLTT 74
|||||
DB 78 VDEKNQVLTT 87
|||||

RESULT 12
T19862
hypothetical protein C40C9.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T19862
R;Hemby, C.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19188
A;Accession: T19862
A;Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A;Residues: 1-542 <WIL>
A;Cross-references: EMBL:Z70266; PIDN:CAA94206.1; GSPDB:GN00028; CESP:C40C9.2
A;Experimental source: Clone C40C9
C;Genetics:
A;Gene: CESP:C40C9.2
A;Map position: X
A;Intons: 11/3; 69/3; 123/2; 173/3; 216/1; 248/1; 279/1; 314/1; 350/3; 430/1; 464/1; 49

Query Match 2.0%; Score 10; DB 2; Length 542;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 RRTLYYGLNL 237
|||||
DB 242 RRTLYYGLNL 251
|||||

RESULT 13
T16652
hypothetical protein R02E12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 19-May-2000
C;Accession: T16652
R;Leinbach, D.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid R02E12.
A;Reference number: Z18554
A;Accession: T16652
A;Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A;Residues: 1-336 <LEI>
A;Cross-references: EMBL:U53337; NID:g1255833; PID:g1255839; PIDN:AAA96188.1; GSPDB:GN00

C;Genetics:
A;Gene: CESP:R02E12.1
A;Map position: X
A;Intons: 11/3; 26/3; 138/1; 183/2; 222/1; 251/1
C;Superfamily: acetylcholine receptor

Query Match 1.8%; Score 9; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 PDILLYNSA 118
|||||
DB 58 PDILLYNSA 66
|||||

RESULT 14
PC4296
nicotinic acetylcholine receptor alpha chain - nematode (Trichostrongylus colubriformis)
N;Alternate names: tar-1 protein
C;Species: Trichostrongylus colubriformis
C;Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Aug-1998
C;Accession: PC4296
R;Wiley, L.J.; Weiss, A.S.; Sangster, N.C.; Li, Q.
Gene 182, 97-100, 1996
A;Title: Cloning and sequence analysis of the candidate nicotinic acetylcholine receptor
A;Reference number: PC4296; MUID:97136696; PMID:8982073
A;Accession: PC4296
A:Molecule type: DNA
A;Residues: 1-466 <WIL>
A;Cross-references: GB:U56903
C;Genetics:
A;Gene: tar-1
C;Superfamily: acetylcholine receptor
F;214-239/Domain: transmembrane #status predicted <TM1>
F;247-270/Domain: transmembrane #status predicted <TM2>
F;276-299/Domain: transmembrane #status predicted <TM3>
F;415-436/Domain: transmembrane #status predicted <TM4>

Query Match 1.8%; Score 9; DB 2; Length 466;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 IDVRWFPPD 160
|||||
DB 110 IDVRWFPPD 118
|||||

RESULT 15
S68588
nicotinic acetylcholine receptor alpha-1 chain precursor (clone Ce21) - Caenorhabditis
C;Species: Caenorhabditis elegans
C;Date: 06-Dec-1996 #sequence_revision 07-Feb-1997 #text_change 20-Aug-1999
C;Accession: S68588; S57496
R;Ballivet, M.; Alliod, C.; Bertrand, S.; Bertrand, D.
J. Mol. Biol. 258, 261-269, 1996
A;Title: Nicotinic acetylcholine receptors in the nematode Caenorhabditis elegans.
A;Reference number: S68587; MUID:96196478; PMID:8627624
A;Accession: S68588
A;Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A;Residues: 1-498 <BAL>
A;Cross-references: EMBL:X83887; NID:g872087; PIDN:CAA58764.1; PID:g872088
C;Superfamily: acetylcholine receptor
C;Keywords: Glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-498/Product: nicotinic acetylcholine receptor alpha-1 chain #status predicted <MAT

Query Match 1.8%; Score 9; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 MRRRTLYYG 234
|||||

Db 225 MRRRTLYG 233

Search completed: June 20, 2003, 19:14:28
Job time : 44 secs

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OM protein - protein search, using sw model

Run on: June 20, 2003, 19:13:47 ; Search time 50 Seconds
(without alignments)
1086.396 Million cell updates/sec

Title: US-09-954-936-2
Perfect score: 502
Sequence: 1 MRCSPGGVWLAALASLLHVS.....TIGILMSAPNFVAVSKDFA 502

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 417779 seqs, 108206813 residues

Word size : 6

Total number of hits satisfying chosen parameters: 2305

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	502	100.0	502	US-09-954-936-2	Sequence 2, Appli
2	401	79.9	502	US-09-892-985-8	Sequence 8, Appli
3	47	9.4	63	US-10-106-698-5644	Sequence 5644, Ap
4	45	9.0	70	US-09-899-495-87	Sequence 87, Appl
5	32	6.4	32	US-09-928-636A-25	Sequence 25, Appl
6	32	6.4	32	US-09-928-636A-27	Sequence 27, Appl
7	20	4.0	20	US-09-928-636A-6	Sequence 6, Appli
8	18	3.6	18	US-09-928-636A-5	Sequence 5, Appli
9	18	3.6	18	US-09-928-636A-8	Sequence 8, Appli
10	15	3.0	15	US-09-928-636A-10	Sequence 4, Appli
11	15	3.0	15	US-09-928-636A-18	Sequence 18, Appl
12	11	2.2	11	US-09-928-636A-7	Sequence 7, Appli
13	11	2.2	11	US-09-928-636A-9	Sequence 9, Appli
14	11	2.2	11	US-09-928-636A-19	Sequence 19, Appl
15	10	2.0	11	US-09-928-636A-10	Sequence 10, Appl
16	10	2.0	11	US-09-928-636A-17	Sequence 17, Appl
17	9	1.8	11	US-09-928-636A-3	Sequence 3, Appli
18	9	1.8	11	US-09-928-636A-11	Sequence 11, Appl
19	9	1.8	450	US-10-156-239-11	Sequence 11, Appl

20	9	1.8	450	9	US-10-199-485-11	Sequence 11, Appl
21	9	1.8	450	10	US-09-795-893-11	Sequence 11, Appl
22	8	1.6	11	9	US-09-928-636A-1	Sequence 1, Appli
23	8	1.6	11	9	US-09-928-636A-16	Sequence 16, Appl
24	8	1.6	245	9	US-09-895-913A-48	Sequence 48, Appl
25	8	1.6	431	10	US-09-835-270-4	Sequence 4, Appli
26	7	1.4	11	9	US-09-928-636A-2	Sequence 2, Appli
27	7	1.4	11	9	US-09-928-636A-12	Sequence 12, Appl
28	7	1.4	28	9	US-09-749-637A-301	Sequence 301, App
29	7	1.4	29	9	US-09-983-802-184	Sequence 184, App
30	7	1.4	37	9	US-09-983-802-399	Sequence 399, App
31	7	1.4	62	10	US-09-864-761-48905	Sequence 48905, A
32	7	1.4	70	9	US-09-749-637A-300	Sequence 300, App
33	7	1.4	73	9	US-10-051-643-141	Sequence 141, App
34	7	1.4	73	9	US-09-880-505-141	Sequence 141, App
35	7	1.4	79	10	US-09-881-752A-20	Sequence 20, Appl
36	7	1.4	84	9	US-10-050-704-134	Sequence 134, App
37	7	1.4	95	9	US-10-023-282-314	Sequence 314, App
38	7	1.4	157	9	US-10-046-938-4	Sequence 4, Appli
39	7	1.4	174	10	US-09-818-066-45	Sequence 45, Appl
40	7	1.4	174	10	US-09-818-066-48	Sequence 48, Appl
41	7	1.4	194	9	US-10-043-487-391	Sequence 391, App
42	7	1.4	213	9	US-10-043-487-374	Sequence 374, App
43	7	1.4	268	10	US-09-823-038A-14	Sequence 14, Appl
44	7	1.4	269	12	US-10-001-843-192	Sequence 192, App
45	7	1.4	289	9	US-10-043-487-299	Sequence 299, App

ALIGNMENTS

RESULT 1
US-09-954-936-2
; Sequence 2, Application US/09954936
; Publication No. US20030073161A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Clark A.
; APPLICANT: Gopalakrishnan, Murali
; APPLICANT: McKenna, David G.
; APPLICANT: Monteggia, Lisa M.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Sullivan, James P.
; APPLICANT: Touma, Edward
; APPLICANT: Abbott Laboratories
; TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE
; FILE REFERENCE: 6017.US.01
; CURRENT APPLICATION NUMBER: US/09/954,936
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 08/771,737
; PRIOR FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 502
; TYPE: PRT
; ORGANISM: homo sapien
US-09-954-936-2

Query Match	100.0%;	Score 502;	DB 9;	Length 502;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 502;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MRCSPGGVWLAALASLLHVS	QGFQRKLYKELVKNYNPLRPVANDSQPTVTVFSLL	60
Db	1	MRCSPGGVWLAALASLLHVS	QGFQRKLYKELVKNYNPLRPVANDSQPTVTVFSLL	60
Qy	61	QIMDVEDKNOVLTTNIWLQMSWTDHYLQWNVSEYGVKTRPPDQIWKPDILLYNSADE	120	
Db	61	QIMDVEDKNOVLTTNIWLQMSWTDHYLQWNVSEYGVKTRPPDQIWKPDILLYNSADE	120	
Qy	121	RFDATEHTNVLNNSGHCQVLPKGIKSSCYDVRWFPEDVQHCCKLFGSGWSYGSJDL	180	

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Db 121 RFDAFHTNVLVNSGHCQYLPGIFKSSCYIDVRWFFPDVQHCCLKFGSWSYGGWSL 180
Qy 181 QMQEADISGYPNGEWDLVGIPGKRSERFYECCKEYPDPVTFVTMRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYPNGEWDLVGIPGKRSERFYECCKEYPDPVTFVTMRRRTLYYGLNLLIP 240
Qy 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS 300
Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS 300
Qy 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKVRPACOKH 360
Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKVRPACOKH 360
Qy 361 QRRCSLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPPTPDSGVVCGRMACSPTHDEHL 420
Qy 421 LHGGQPPGDPDLAKILEEVRYIANFRFCODESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPGDPDLAKILEEVRYIANFRFCODESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

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RESULT 2

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US-09-892-985-8
; Sequence 8, Application US/09892985
; Patent No. US20020111463A1
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/892,985
; FILING DATE: 27-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-98
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/466,589,
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9949B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-587-5360
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-892-985-8

Query Match 79.9%; Score 401; DB 10; Length 502;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRCSPGGVWALAAASLLHVSLSQGEFQKLYKELVKNYNPLRPVANDSQBLTVYFSL 60
Db 1 MRCSPGGVWALAAASLLHVSLSQGEFQKLYKELVKNYNPLRPVANDSQBLTVYFSL 60
Qy 61 QIMDVDEKQVLTNINWLSWTDHYLOMNVSEYVPGVKTFRFPDQGIWKPDILLYNSADE 120
Db 61 QIMDVDEKQVLTNINWLSWTDHYLOMNVSEYVPGVKTFRFPDQGIWKPDILLYNSADE 120
Qy 121 RFDAFHTNVLVNSGHCQYLPGIFKSSCYIDVRWFFPDVQHCCLKFGSWSYGGWSL 180
Db 121 RFDAFHTNVLVNSGHCQYLPGIFKSSCYIDVRWFFPDVQHCCLKFGSWSYGGWSL 180
Qy 181 QMQEADISGYPNGEWDLVGIPGKRSERFYECCKEYPDPVTFVTMRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYPNGEWDLVGIPGKRSERFYECCKEYPDPVTFVTMRRRTLYYGLNLLIP 240
Qy 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS 300
Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS 300
Qy 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKVRPACOKH 360
Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKVRPACOKH 360
Qy 361 QRRCSLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPPTPDSGVVCGRMACSPTHDEHL 420
Qy 421 LHGGQPPGDPDLAKILEEVRYIANFRFCODESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPGDPDLAKILEEVRYIANFRFCODESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 3
US-10-106-698-5644
; Sequence 5644, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 5644
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)

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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (8)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (12)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (16)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-106-698-5644

Query Match 9.4%; Score 47; DB 9; Length 63;
Best Local Similarity 100.0%; Pred. No. 4.8e-38;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 456 VCSEWFAACVDRCLCMASFVFTIICIGILMSAPNFVEAVSKDFA 502
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Db 17 VCSEWFAACVDRCLCMASFVFTIICIGILMSAPNFVEAVSKDFA 63
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RESULT 4

US-09-899-495-87
; Sequence 87, Application US/09899495
; Publication No. US20030088060A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Christopher W.
; APPLICANT: Roberts, Steven L.
; APPLICANT: Karnovsky, Alla M.
; APPLICANT: Ruble, Cara L.
; TITLE OF INVENTION: Human Ion Channels
; FILE REFERENCE: 00188US1
; CURRENT APPLICATION NUMBER: US/09/899,495
; PRIORITY FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/215,815
; PRIORITY FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: 60/216,481
; PRIORITY FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 60/216,479
; PRIORITY FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 60/216,482
; PRIORITY FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 60/217,096
; PRIORITY FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 87
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-899-495-87

Query Match 9.0%; Score 45; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 4.7e-36;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 413 SPTHDEHLHGQPPGDPDLAKILEEVRYIANFRQDSEAVC 457
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Db 1 SPTHDEHLHGQPPGDPDLAKILEEVRYIANFRQDSEAVC 45
|||||

RESULT 5

US-09-928-636A-25
; Sequence 25, Application US/09928636A
; Publication No. US20030092613A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Daniel H
; APPLICANT: Wang, Hoau-Yan
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Reitz, Allen B

; TITLE OF INVENTION: alpha7 nicotinic receptor peptides as ligands for beta
; FILE REFERENCE: beta amyloid binding peptides
; CURRENT APPLICATION NUMBER: US/09/928,636A
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 25
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-928-636A-25

Query Match 6.4%; Score 32; DB 9; Length 32;
Best Local Similarity 100.0%; Pred. No. 1e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 NGEWDLVGIPGKRSERFYECCKEYPDVTFV 224
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Db 1 NGEWDLVGIPGKRSERFYECCKEYPDVTFV 32
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RESULT 6

US-09-928-636A-27
; Sequence 27, Application US/09928636A
; Publication No. US20030092613A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Daniel H
; APPLICANT: Wang, Hoau-Yan
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Reitz, Allen B
; TITLE OF INVENTION: alpha7 nicotinic receptor peptides as ligands for beta
; FILE REFERENCE: beta amyloid peptides
; CURRENT APPLICATION NUMBER: US/09/928,636A
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 27
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-928-636A-27

Query Match 6.4%; Score 32; DB 9; Length 32;
Best Local Similarity 100.0%; Pred. No. 1e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 SGYIPNGEWDLVGIPGKRSERFYECCKEYPD 219
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Db 1 SGYIPNGEWDLVGIPGKRSERFYECCKEYPD 32
|||||

RESULT 7

US-09-928-636A-6
; Sequence 6, Application US/09928636A
; Publication No. US20030092613A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Daniel H
; APPLICANT: Wang, Hoau-Yan
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Reitz, Allen B
; TITLE OF INVENTION: alpha7 nicotinic receptor peptides as ligands for beta
; FILE REFERENCE: beta amyloid peptides
; CURRENT APPLICATION NUMBER: US/09/928,636A
; CURRENT FILING DATE: 2001-08-13

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; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-928-636A-6

Query Match          4.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.3e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 IPGKRSERFYECCKEPYDV 220
Db 1 IPGKRSERFYECCKEPYDV 20

RESULT 8
US-09-928-636A-5
; Sequence 5, Application US/09928636A
; Publication No. US20030092613A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Daniel H
; APPLICANT: Wang, Hoau-Yan
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Reitz, Allen B
; TITLE OF INVENTION: alpha7 nicotinic receptor peptides as ligands for beta
; TITLE OF INVENTION: amyloid peptides
; FILE REFERENCE: beta amyloid binding peptides
; CURRENT APPLICATION NUMBER: US/09/928,636A
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-928-636A-5

Query Match          3.6%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 IPGKRSERFYECCKEPYDV 218
Db 1 IPGKRSERFYECCKEPYDV 18

RESULT 9
US-09-928-636A-8
; Sequence 8, Application US/09928636A
; Publication No. US20030092613A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Daniel H
; APPLICANT: Wang, Hoau-Yan
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Reitz, Allen B
; TITLE OF INVENTION: alpha7 nicotinic receptor peptides as ligands for beta
; TITLE OF INVENTION: amyloid peptides
; FILE REFERENCE: beta amyloid binding peptides
; CURRENT APPLICATION NUMBER: US/09/928,636A
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-928-636A-8

Query Match          3.6%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 IPGKRSERFYECCKEPYDV 227
Db 1 YECCKEYPDVFTVTMR 18

RESULT 10
US-09-928-636A-4
; Sequence 4, Application US/09928636A
; Publication No. US20030092613A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Daniel H
; APPLICANT: Wang, Hoau-Yan
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Reitz, Allen B
; TITLE OF INVENTION: alpha7 nicotinic receptor peptides as ligands for beta
; TITLE OF INVENTION: amyloid peptides
; FILE REFERENCE: beta amyloid binding peptides
; CURRENT APPLICATION NUMBER: US/09/928,636A
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-928-636A-4

Query Match          3.0%; Score 15; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 200 GIPGKRSERFYECCCK 214
Db 1 GIPGKRSERFYECCCK 15

RESULT 11
US-09-928-636A-18
; Sequence 18, Application US/09928636A
; Publication No. US20030092613A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Daniel H
; APPLICANT: Wang, Hoau-Yan
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Reitz, Allen B
; TITLE OF INVENTION: alpha7 nicotinic receptor peptides as ligands for beta
; TITLE OF INVENTION: amyloid peptides
; FILE REFERENCE: beta amyloid binding peptides
; CURRENT APPLICATION NUMBER: US/09/928,636A
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-928-636A-18
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Query Match 3.0%; Score 15; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 200 GIPGKRSERFYECCK 214
Db 1 GIPGKRSERFYECCK 15
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RESULT 12
US-09-928-636A-7
; Sequence 7, Application US/09928636A
; Publication No. US20030092613A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Daniel H
; APPLICANT: Wang, Hoau-Yan
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Reitz, Allen B
; TITLE OF INVENTION: alpha7 nicotinic receptor peptides as ligands for beta
; FILE REFERENCE: beta amyloid peptides
; CURRENT APPLICATION NUMBER: US/09/928,636A
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-928-636A-7

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Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 206 SERFYECCKEP 216
Db 1 SERFYECCKEP 11
|||||

RESULT 13
US-09-928-636A-9
; Sequence 9, Application US/09928636A
; Publication No. US20030092613A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Daniel H
; APPLICANT: Wang, Hoau-Yan
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Reitz, Allen B
; TITLE OF INVENTION: alpha7 nicotinic receptor peptides as ligands for beta
; FILE REFERENCE: beta amyloid peptides
; CURRENT APPLICATION NUMBER: US/09/928,636A
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-928-636A-9

Query Match 2.2%; Score 11; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 206 SERFYECCKEP 216
Db 1 SERFYECCKEP 11
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RESULT 14
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; Sequence 19, Application US/09928636A
; Publication No. US20030092613A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Daniel H
; APPLICANT: Wang, Hoau-Yan
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Reitz, Allen B
; TITLE OF INVENTION: alpha7 nicotinic receptor peptides as ligands for beta
; FILE REFERENCE: beta amyloid peptides
; CURRENT APPLICATION NUMBER: US/09/928,636A
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-928-636A-19

Query Match 2.2%; Score 11; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 SERFYECCKEP 11
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RESULT 15
US-09-928-636A-10
; Sequence 10, Application US/09928636A
; Publication No. US20030092613A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Daniel H
; APPLICANT: Wang, Hoau-Yan
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Reitz, Allen B
; TITLE OF INVENTION: alpha7 nicotinic receptor peptides as ligands for beta
; FILE REFERENCE: beta amyloid peptides
; CURRENT APPLICATION NUMBER: US/09/928,636A
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-928-636A-10

Query Match 2.0%; Score 10; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 ERFYECCKEP 216
Db 2 ERFYECCKEP 11
|||||

Fri Jun 27 07:47:22 2003

us-09-954-936-2.oligo.rapb

Page 6

Search completed: June 20, 2003, 19:23:18
Job time : 51 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2003, 19:01:21 ; Search time 73 Seconds
(without alignments)
916.326 Million cell updates/sec

Title: US-09-954-936-2

Perfect score: 502

Sequence: 1 MRCSPGVWLAALASLLHVS.....TIGILMSAPNFVAVSKDPA 502

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 6

Total number of hits satisfying chosen parameters: 3004

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	502	100.0	502	19 AAW69216	V274T variant huma
2	401	79.9	502	15 AAW44153	Human neuronal nic
3	401	79.9	502	18 AAW09025	Neuronal nicotinic
4	401	79.9	502	21 AAB24088	Human PRO2145 prot
5	401	79.9	502	22 AAB82690	Nicotinic acetylch
6	401	79.9	502	22 AAB50012	Wild-type human al
7	300	59.8	502	22 AAB50015	Mutant human alpha
8	300	59.8	502	22 AAB50016	Mutant human alpha
9	229	45.6	502	22 AAB50017	Mutant human alpha
10	224	44.6	470	22 AAB50014	Chimeric alpha7/5-

11	202	40.2	448	22	AAB50018	Mature cell surfac
12	92	18.3	502	18	AAW12368	Neuronal alpha-bun
13	47	9.4	63	22	AAG74870	Human colon cancer
14	45	9.0	70	23	AAU83518	Novel human ion ch
15	32	6.4	32	23	ABW76012	Beta amyloid bindi
16	32	6.4	32	23	ABW76014	Beta amyloid bindi
17	27	5.4	511	18	AAW12369	Neuronal alpha-bun
18	20	4.0	20	23	ABW5993	Beta amyloid bindi
19	18	3.6	18	23	ABW5992	Beta amyloid bindi
20	18	3.6	18	23	ABW5995	Beta amyloid bindi
21	15	3.0	15	23	ABW5991	Beta amyloid bindi
22	15	3.0	15	23	ABW6005	Beta amyloid bindi
23	13	2.6	21	22	AAE10084	Human ion channel
24	11	2.2	11	23	ABW5994	Beta amyloid bindi
25	11	2.2	11	23	ABW5996	Beta amyloid bindi
26	11	2.2	11	23	ABW76006	Beta amyloid bindi
27	10	2.0	11	23	ABW5997	Beta amyloid bindi
28	10	2.0	11	23	ABW76004	Beta amyloid bindi
29	10	2.0	250	22	ABG06105	Novel human diago
30	10	2.0	279	22	AAU87310	Novel central nerv
31	10	2.0	304	22	ABG06104	Novel human diago
32	10	2.0	304	22	ABG06107	Novel human diago
33	10	2.0	457	22	AAB50013	Murine 5HT3 ligand
34	10	2.0	478	23	ABW08137	Human 5-Hydroxytry
35	10	2.0	478	23	AAU79383	Human 5-Hydroxytry
36	10	2.0	479	17	AAR89358	Alpha-9 nicotinic
37	9	1.8	11	23	ABW5990	Beta amyloid bindi
38	9	1.8	11	23	ABW5998	Beta amyloid bindi
39	9	1.8	85	22	AAE10085	Human ion channel
40	9	1.8	382	23	AAE21162	Human TRICH-6 prot
41	9	1.8	433	22	AAU00402	Mature human alpha
42	9	1.8	450	22	AAG67161	Amino acid sequenc
43	9	1.8	450	22	AAU00403	Human alpha nicoti
44	9	1.8	450	22	AAE00280	Human nicotinic ac
45	9	1.8	450	23	AAE21171	Human TRICH-15 pro

ALIGNMENTS

RESULT 1
AAW69216
ID AAW69216 standard; Protein; 502 AA.

XX AC AAW69216;

XX DT 09-OCT-1998 (first entry)

XX DE V274T variant human alpha7 nAChR protein.

XX KW Alpha7 nAChR; alpha7 nicotinic acetylcholine receptor subunit; cancer; neurodegeneration; enzyme dysfunction; affective disorder; therapy; immune dysfunction; diabetic neuropathy; Alzheimer's disease; schizophrenia.

XX OS Homo sapiens.

XX PN W09828331-A2.

XX PD 02-JUL-1998.

XX PF 22-DEC-1997; 97WO-US23405.

XX PR 20-DEC-1996; 96US-0771737.

XX PA (ABBO) ABBOTT LAB.

XX PI Briggs CA, Gopalakrishnan M, McKenna DG, Monteggia LM;

XX PI Roch J, Sullivan JF, Touma E;

XX DR WPI; 1998-377593/32.

XX DR N-PSDB; AAV44687.

PT Nucleic acid encoding variant of human alpha7 nicotinic
PT acetylcholine receptor sub-unit - used to identify modulators of
PT the receptor, potentially useful for treating neuro-degeneration,
XX cancer, affective disorders etc.
PS Claim 15; Fig 2; 44pp; English.
XX
CC This sequence is the V247T variant of human alpha7 nicotinic
CC acetylcholine receptor (NACHR) subunit of the invention. Cells containing
CC the DNA are used to express the protein and to identify modulators of
CC alpha7 NACHR activity or cytoprotective agents, e.g. antisense
CC compounds or antagonists that are potentially useful for treating
CC neurodegeneration, enzyme dysfunction, affective disorders and immune
CC dysfunction, such as cancer, post-herpetic neuralgia, diabetic
CC neuropathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru,
CC psychosis and schizophrenia. Probes based on the DNA are used to detect
CC the DNA in usual hybridisation or amplification tests, while monoclonal
CC antibodies are used to detect the protein for diagnosis (in vitro or by
CC in situ immuno-fluorescent assay). Compared with wild-type alpha7 NACHR,
CC the protein has about 100-fold greater sensitivity to cholinergic
CC receptor agonists (nicotine or acetylcholine) and response to these
CC agonists decays more slowly, but the wild-type inward rectification is
CC retained.
XX
SQ Sequence 502 AA;
Query Match 100.0%; Score 502; DB 19; Length 502;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRCSPGGVWLAASLLHVSQGEFQKLYKELVKNYNPLERPVPANDSQPLTVVFSLSLL 60
DB 1 MRCSPGGVWLAASLLHVSQGEFQKLYKELVKNYNPLERPVPANDSQPLTVVFSLSLL 60
QY 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQMNVSYPGVKTVRFPDQIWKPDILLYNSADE 120
DB 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQMNVSYPGVKTVRFPDQIWKPDILLYNSADE 120
QY 121 RDATFHTNVLNSSGHCQVLPFGIFKSSCYIDVRWFFPDVQHCCKLFGSWSYGGWSLDL 180
DB 121 RDATFHTNVLNSSGHCQVLPFGIFKSSCYIDVRWFFPDVQHCCKLFGSWSYGGWSLDL 180
QY 181 QMQEADISGYPNGEWDLVGIPKGRSERFYECCKEPYDPDVTFTVMRRRTLYGLNLLIP 240
DB 181 QMQEADISGYPNGEWDLVGIPKGRSERFYECCKEPYDPDVTFTVMRRRTLYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFFMLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVTVILOYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKVPACQHK 360
DB 301 MIIVGLSVVTVTVILOYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKVPACQHK 360
QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDSGVCGRMACSPTHDEHL 420
DB 361 QRCCLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDSGVCGRMACSPTHDEHL 420
QY 421 LHGGQPEGDPDLAKILEEYRYIANFRPCODESEAVCSWKFAACVVDRLCLMAFSVFTI 480
DB 421 LHGGQPEGDPDLAKILEEYRYIANFRPCODESEAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 2
AAW44153
ID AAW44153 standard; Protein; 502 AA.
XX
AC AAW44153;
XX

DT 14-MAY-1998 (first entry)
XX Human neuronal nicotinic acetylcholine receptor alpha-7 subunit.
DE
XX
XX Human neuronal nicotinic acetylcholine receptor; alpha-7 subunit;
KW brain tissue; screening; NACHR; antibody.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FT Peptide 1..23
FT /label= signal
FT Domain 229..256
FT /label= TMD1
FT /note= "transmembrane domain"
FT Domain 262..284
FT /label= TMD2
FT /note= "transmembrane domain"
FT Domain 290..317
FT /label= TMD3
FT /note= "transmembrane domain"
FT Misc-difference 343
FT /note= "encoded by CTS"
FT Domain 462..487
FT /label= TMD4
FT /note= "transmembrane domain"
FT Domain 318..461
FT /label= cytoplasmic_loop
XX
PN WO9420617-A2.
XX
XX 15-SEP-1994.
XX
XX 08-MAR-1994; 94WO-US02447.
XX
XX 08-MAR-1993; 93US-0028031.
XX
XX (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
XX (SIBI-) SIBIA NEUROSCIENCES INC.
XX
XX Elliott KJ, Ellis SB, Harpold MM;
XX
XX WPI; 1994-303024/37.
XX N-PSDB; AAV12197.
XX
XX Human neuronal nicotinic acetylcholine receptor subunits and DNA -
XX also transformed cells useful for screening cpds. which modulate
XX activity of the receptor
XX
XX Claim 7; Page 80-81; 99pp; English.
XX
XX The present sequence represents a human neuronal nicotinic acetylcholine
XX receptor (NACHR) subunit. The cells expressing the alpha and/or beta
XX NACHR subunits may be used in a method of screening compounds to
XX identify any which modulate the activity of human neuronal NACHR.
XX Subunit specific antibodies may be used to monitor the distribution
XX and expression density of various subunits in normal vs diseased brain
XX tissues. Testing of single receptor subunits or specific receptor
XX subunit combinations with a variety of potential agonists or antagonists
XX provides information with respect to the function and activity of the
XX individual subunits and should lead to the identification and design of
XX compounds that are capable of very specific interaction with one or
XX more receptor subtypes. The resulting drugs should exhibit fewer
XX unwanted side effects than drugs identified e.g. screening with cells
XX that express a variety of subtypes.
XX
SQ Sequence 502 AA;
Query Match 79.9%; Score 401; DB 15; Length 502;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRCSPGGVWLAASLLHVSQGEFQKLYKELVKNYNPLERPVPANDSQPLTVVFSLSLL 60


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Db      1 MRCSPGGVWLAALASLLHVSLSQGFQRLKYELVKNYNPLRPVANDSQPLTVYFSL 60
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Db      61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQMNVSYPGVKTVRPPDQGIWKPDILLYNSADE 120
QY      121 RFDATEHTNNLVNNSGHCQVLPFGIFKSSCYIDVRWFFPDVQHCCLKFGSWSYGWSL 180
Db      121 RFDATEHTNNLVNNSGHCQVLPFGIFKSSCYIDVRWFFPDVQHCCLKFGSWSYGWSL 180
QY      181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFVTMRRTLYYGLNLLIP 240
Db      181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFVTMRRTLYYGLNLLIP 240
QY      241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db      241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY      301 MIIVGLSVVTVTVIQLYHHDDPDGKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
Db      301 MIIVGLSVVTVTVIQLYHHDDPDGKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
QY      361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db      361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY      421 LHGGQPPGDPDLAKILEEVRYIANRFRQDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
Db      421 LHGGQPPGDPDLAKILEEVRYIANRFRQDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
QY      481 ICTIGILMSAPNFVEAVSKDFA 502
Db      481 ICTIGILMSAPNFVEAVSKDFA 502

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RESULT 3

```

AAW09025
ID AAW09025 standard; Protein; 502 AA.
AC AAW09025;
XX
DT 09-APR-1997 (first entry)
DE Neuronal nicotinic acetylcholine receptor alpha-7 subunit.
KW Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
KW ligand-gated receptor.
XX
OS Homo sapiens.
XX
PN WO9641876-A1.
XX
PD 27-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US09775.
XX
PR 07-JUN-1995; 95US-0484722.
XX
PA (SIBI-) SIBIA NEUROSCIENCES INC.
XX
PI Elliott KJ, Harpold MW;
XX
DR WPI, 1997-065463/06.
DR N-PSDB; AAT48239.
XX
PT Nucleic acids encoding nicotinic acetylcholine receptor sub-units -
PT used in screening to determine the effect of drugs on the receptor
XX
PS Disclosure; Page 73-74; 108pp; English.
XX
CC The alpha-7 subunit (AAW09025) of the human neuronal nicotinic
CC acetylcholine receptor (nAChR) can be expressed in transformed

```

```

CC host cells carrying alpha-7 subunit DNA (see also AAT48239). Host
CC cells, esp. mammalian cells or amphibian oocytes, expressing the
CC recombinant alpha-7 subunit, opt. in combination with other
CC recombinant alpha and/or beta subunits (see also AAW09018-24,
CC AAW09026-27), can be used to examine the function of human AChR and
CC to identify cpds. that modulate its activity.
XX
SQ Sequence 502 AA;

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Query Match 79.9%; Score 401; DB 18; Length 502;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MRCSPGGVWLAALASLLHVSLSQGFQRLKYELVKNYNPLRPVANDSQPLTVYFSL 60
QY 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQMNVSYPGVKTVRPPDQGIWKPDILLYNSADE 120
Db 61 QIMDVDEKNQVLTNNIWLQMSWTDHYLQMNVSYPGVKTVRPPDQGIWKPDILLYNSADE 120
QY 121 RFDATEHTNNLVNNSGHCQVLPFGIFKSSCYIDVRWFFPDVQHCCLKFGSWSYGWSL 180
Db 121 RFDATEHTNNLVNNSGHCQVLPFGIFKSSCYIDVRWFFPDVQHCCLKFGSWSYGWSL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFVTMRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFVTMRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVTVIQLYHHDDPDGKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
Db 301 MIIVGLSVVTVTVIQLYHHDDPDGKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPGDPDLAKILEEVRYIANRFRQDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPGDPDLAKILEEVRYIANRFRQDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

```

RESULT 4

```

AAB24088
ID AAB24088 standard; Protein; 502 AA.
AC AAB24088;
XX
DT 29-JAN-2001 (first entry)
DE Human PRO2145 protein sequence SEQ ID NO:77.
XX
KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW proliferation; tumorigenesis; identification; cancer; cytostatic;
KW neurotropic; neuroprotective; antiinflammatory; immunosuppressive;
KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
KW neuronal disorder; glial disorder; astrocytoma; angiogenic;
KW hypothalamic disorder; glandular disorder; macrophage disorder;
KW epithelial disorder; stromal disorder; blastocoele disorder;
KW inflammatory disorder; immunologic disorder.
XX
OS Homo sapiens.
XX
PN WO200053755-A2.
XX

```

PD 14-SEP-2000.
 XX
 PF 06-JAN-2000; 2000WO-US00376.
 XX
 PR 08-MAR-1999; 99WO-US05028.
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 07-JUL-1999; 99US-0143048.
 PR 26-JUL-1999; 99US-0145698.
 PR 30-NOV-1999; 99WO-US28313.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US00219.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
 PI Watanabe CK, Wood WI;
 XX
 DR WPI; 2000-572270/53.
 DR N-PSDB; AAC58395.
 XX
 PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
 PT treatment, diagnosis and prevention of cancer -
 XX
 PS Claim 61; Fig 58; 286pp; English.
 XX
 CC The present invention describes an isolated antibody that binds to
 CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,
 CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,
 CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,
 CC PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,
 CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell
 CC growth. The PRO polypeptides and nucleotides are useful in the
 CC treatment, diagnosis and prevention of cancer. The antibodies and other
 CC anti-tumour compounds may be used to treat various conditions, including
 CC those characterised by overexpression and/or activation of the amplified
 CC PRO genes. Exemplary conditions or disorders to be treated with such
 CC antibodies and other compounds include benign or malignant tumours
 CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,
 CC colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic
 CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours),
 CC leukaemias and lymphoid malignancies, other disorders such as neuronal,
 CC glial, astrocytic, hypothalamic and other glandular, macrophagal,
 CC epithelial, stromal and blastocoele disorders, and inflammatory,
 CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR
 CC primers and hybridisation probes used in the isolation of the human PRO
 CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human
 CC PRO polynucleotide and protein sequences given in the exemplification of
 CC the present invention.
 XX
 XX Sequence 502 AA;
 SQ
 Query Match 79.9%; Score 401; DB 21; Length 502;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MRCSPGGWLAAALSHVLSQGEFQKLYKELVKNVNPVANDSQPLTVFSL 60
 DB 1 MRCSPGGWLAAALSHVLSQGEFQKLYKELVKNVNPVANDSQPLTVFSL 60
 QY 61 QIMDVDEKQVLTNTLWQSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILYNSADE 120
 DB 61 QIMDVDEKQVLTNTLWQSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILYNSADE 120
 QY 121 RFDATHTNVLNNSGHCQYLPFGIFKSSCYIDVRWPFDFVQHCXKAFGWSYGSWLSLDL 180
 DB 121 RFDATHTNVLNNSGHCQYLPFGIFKSSCYIDVRWPFDFVQHCXKAFGWSYGSWLSLDL 180
 QY 181 QMQEADISGYPNGEWDLVGIPGKRSRFEYCKEPEYDVTFTVTRRRTLYYGLNLLIP 240
 DB 181 QMQEADISGYPNGEWDLVGIPGKRSRFEYCKEPEYDVTFTVTRRRTLYYGLNLLIP 240
 QY 241 CVLISALALVFLPADSGEKISLGITVLLSLTFVFMLLVAEIMPATSDSVPLIAQYFAST 300

Db 241 CVLISALALVFLPADSGEKISLGITVLLSLTFVFMLLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVTVIVLQYHHHDPDGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHK 360
 Db 301 MIIVGLSVVTVIVLQYHHHDPDGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHK 360
 QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
 Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
 QY 421 LHGQPPGPDPAKILEEVRYIANRPRCODESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
 Db 421 LHGQPPGPDPAKILEEVRYIANRPRCODESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 Db 481 ICTIGILMSAPNFVEAVSKDFA 502
 RESULT 5
 AAB82690
 ID AAB82690 standard; Protein; 502 AA.
 XX
 AC AAB82690;
 XX
 DT 15-OCT-2001 (first entry)
 XX
 DE Nicotinic acetylcholine receptor alpha7.
 XX
 KW Nicotinic acetylcholine receptor; nAChR; human;
 KW acetylcholine binding protein; AChBP; mollusc;
 KW ligand-binding protein; ligand-gated ion channel; crystal;
 KW drug design; protein co-ordinate data; schizophrenia;
 KW Alzheimer's disease; nicotine addiction; Tourette's syndrome;
 KW therapy; nootropic; neuroprotective.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 108..115
 FT /note= "conserved ligand-binding region, residues
 FT Trp108 and Tyr115 are essential"
 FT Region 171..173
 FT /note= "conserved ligand-binding region, residues
 FT Trp171 and Tyr173 are essential"
 FT Region 210..217
 FT /note= "conserved ligand-binding region, residues
 FT Tyr210, Cys212, Cys213 and Tyr217 are
 FT essential"
 XX
 FN WO200158951-A2.
 XX
 PD 16-AUG-2001.
 XX
 DP 09-FEB-2001; 2001WO-EP01457.
 XX
 PR 10-FEB-2000; 2000EP-0200443.
 PR 31-OCT-2000; 2000EP-0203810.
 XX
 PA (TEWE-) STICHTING TECH WETENSCHAPPEN.
 XX
 PI Smit AB, Sixma TK;
 XX
 DR WPI; 2001-497071/54.
 XX
 PT Water-soluble ligand-binding proteins derived from molluscs and analogues
 PT of ligand-gated ion channels, useful in drug screening assay, where the
 PT drugs identified can be used in the treatment of Alzheimer's disease or
 PT schizophrenia -
 XX
 PS Disclosure; Page 252-254; 260pp; English.

CC The present sequence is that of the alpha subunit of human
CC nicotinic acetylcholine receptor (nAChR). The sequence includes
CC regions that are conserved throughout the various nAChR alpha
CC subunits and which are essential for ligand binding. The invention
CC relates to water-soluble ligand-binding proteins derived from
CC molluscs, especially acetylcholine-binding proteins (AChBPs) and
CC analogues of ligand-gated ion channels, their crystals, and their
CC use for screening ligands of ligand-gated ion channels. The
CC water-soluble ligand-binding proteins are capable of forming
CC multimers and are amenable to crystallization. The crystal
CC structure of AChBP is provided, and can be used to generate 3D
CC models of the extracellular ligand-binding domain of ligand-gated
CC ion channels and thus for screening of drugs that act on these
CC ion channels. Chimeric proteins are provided that are capable of
CC binding a ligand of a ligand-gated receptor, and comprise at
CC least the amino acids of the AChBP determining solubility of the
CC AChBP, in the same positions as in the AChBP, and also comprising
CC amino acids determining binding to the ligand. In the chimeric
CC proteins, at least the essential amino acids of at least 1 of the
CC conserved regions of an nAChR have been substituted for the
CC corresponding amino acids, and preferably entire stretches have
CC been substituted. New drugs can be developed that selectively
CC intervene in neuronal signalling pathways, especially where the
CC ligand-gated ion channel is the nAChR, and the related disorder is
CC Tourette's syndrome, Alzheimer's disease, addiction to nicotine
CC or schizophrenia.
XX
SQ Sequence 502 AA;

Query Match 79.9%; Score 401; DB 22; Length 502;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRCSPGGVWLAALASLLHVSLLQGEFQRLKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
Db 1 MRCSPGGVWLAALASLLHVSLLQGEFQRLKLYKELVKNYNPLRPVANDSQPLTVYFSL 60

Qy 61 QIMDVEKNQVLTNNIWLQMSWTDHYLQMNVSYPGVKTRFPDQGIWKPDILLYNSADE 120
Db 61 QIMDVEKNQVLTNNIWLQMSWTDHYLQMNVSYPGVKTRFPDQGIWKPDILLYNSADE 120

Qy 121 RPDATHTNNVLSNGSHCQVLPDGIKSSCYIDVRWPFDFVQHCKLFGSGWSYGGSLDL 180
Db 121 RPDATHTNNVLSNGSHCQVLPDGIKSSCYIDVRWPFDFVQHCKLFGSGWSYGGSLDL 180

Qy 181 QMQEADISGYIPNGEWDLVGIPGRSRFYECCKEPYDVTFTVMRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGRSRFYECCKEPYDVTFTVMRRRTLYYGLNLLIP 240

Qy 241 CVLISALALLVFLLPADSGEKISLGITVLLSLTFFMLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLLPADSGEKISLGITVLLSLTFFMLVAEIMPATSDSVPLIAQYFAST 300

Qy 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCAMFLRMKRPGEKVRPACQHK 360
Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCAMFLRMKRPGEKVRPACQHK 360

Qy 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420

Qy 421 LHGGQPPEGDPDLAKILEEVRYTANRRCODESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYTANRRCODESEAVCSWKFAACVVDRLCLMAFSVFTI 480

Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 6
AAB50012
ID AAB50012 standard; Protein; 502 AA.

XX AAB50012;
AC 14-WAR-2001 (first entry)
DT Wild-type human alpha7 ligand gated ion channel.
DE Human; alpha7 nicotinic acetylcholine gated ion channel;
KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance.
XX Homo sapiens.
PN WO200073431-A2.
XX 07-DEC-2000.
PF 25-MAY-2000; 2000WO-US11862.
XX 27-MAY-1999; 99US-0136174.
PA (PHAA) PHARMACIA & UPJOHN CO.
PI Groppi VE, Wolfe ML, Berkenpas MB;
XX WPI; 2001-061524/07.
DR N-PSDB; AAC90380.
PT Special cell culture medium for treating cells and for inducing
PT mammalian cell lines to conduct calcium ions, comprising specified
PT concentrations of ions of sodium, calcium and potassium at specified pH
XX
PS Disclosure; Pages 61-63; 77pp; English.
CC The present sequence is wild-type human alpha7 nicotinic acetylcholine
CC gated ion channel. The human alpha7 ion channel was used in the
CC construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand
CC gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric
CC ion channel can be expressed by recombinant cells in the present
CC invention, resulting in preferential calcium ion conductance by the
CC cells.
XX
SQ Sequence 502 AA;

Query Match 79.9%; Score 401; DB 22; Length 502;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRCSPGGVWLAALASLLHVSLLQGEFQRLKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
Db 1 MRCSPGGVWLAALASLLHVSLLQGEFQRLKLYKELVKNYNPLRPVANDSQPLTVYFSL 60

Qy 61 QIMDVEKNQVLTNNIWLQMSWTDHYLQMNVSYPGVKTRFPDQGIWKPDILLYNSADE 120
Db 61 QIMDVEKNQVLTNNIWLQMSWTDHYLQMNVSYPGVKTRFPDQGIWKPDILLYNSADE 120

Qy 121 RPDATHTNNVLSNGSHCQVLPDGIKSSCYIDVRWPFDFVQHCKLFGSGWSYGGSLDL 180
Db 121 RPDATHTNNVLSNGSHCQVLPDGIKSSCYIDVRWPFDFVQHCKLFGSGWSYGGSLDL 180

Qy 181 QMQEADISGYIPNGEWDLVGIPGRSRFYECCKEPYDVTFTVMRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGRSRFYECCKEPYDVTFTVMRRRTLYYGLNLLIP 240

Qy 241 CVLISALALLVFLLPADSGEKISLGITVLLSLTFFMLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLLPADSGEKISLGITVLLSLTFFMLVAEIMPATSDSVPLIAQYFAST 300

Qy 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCAMFLRMKRPGEKVRPACQHK 360
Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCAMFLRMKRPGEKVRPACQHK 360

Qy 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420

Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
 QY 421 LHGGQPEGDPDLAKILEEVRYIANRPRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 Db 421 LHGGQPEGDPDLAKILEEVRYIANRPRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 7
 AAB50015
 ID AAB50015 standard; Protein; 502 AA.
 AC AAB50015;
 XX
 DT 14-MAR-2001 (first entry)
 DE Mutant human alpha7 ligand gated ion channel #1.
 KW Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;
 XX 5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutein.
 OS Homo sapiens.
 XX Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 230
 FT /note= "Wild-type Thr substituted by Pro"
 XX
 PN WO200073431-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 25-MAY-2000; 2000WO-US11862.
 XX
 PR 27-MAY-1999; 99US-0136174.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Groppi VE, Wolfe ML, Berkenpas MB;
 XX
 DR WPI; 2001-061524/07.
 DR N-PSDB; AAC90385.
 XX
 PT Special cell culture medium for treating cells and for inducing
 PT mammalian cell lines to conduct calcium ions, comprising specified
 PT concentrations of ions of sodium, calcium and potassium at specified pH
 XX
 XX
 XX Claim 100; Pages 70-72; 77pp; English.
 PS
 CC The present sequence is a mutant human alpha7 nicotinic acetylcholine
 CC gated ion channel. The human alpha7 ion channel was used in the
 CC construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand
 CC gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric
 CC ion channel can be expressed by recombinant cells in the present
 CC invention, resulting in preferential calcium ion conductance by the
 CC cells.
 XX
 XX Sequence 502 AA;
 SQ
 Query Match 59.8%; Score 300; DB 22; Length 502;
 Best Local Similarity 99.6%; Pred. No. 2.8e-282;
 Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MRCSPGGVWLAASLLHVSLSQGFQRLKYLKELVKNYNPLRPVANDSQPLTVVFSLSLL 60
 Db 1 MRCSPGGVWLAASLLHVSLSQGFQRLKYLKELVKNYNPLRPVANDSQPLTVVFSLSLL 60
 QY 61 QIMDVDEKNQVLTNIWLQMSWTDHYLQMNVSYPGVKTVRFPDQIWKPDILLYNSADE 120

Db 61 QIMDVDEKNQVLTNIWLQMSWTDHYLQMNVSYPGVKTVRFPDQIWKPDILLYNSADE 120
 QY 121 RFDPATFTNVLNNSGHCQYLPGCIFKSSCYIDVRNPFDDVQHCKLFGSWSYGGWSL 180
 Db 121 RFDPATFTNVLNNSGHCQYLPGCIFKSSCYIDVRNPFDDVQHCKLFGSWSYGGWSL 180
 QY 181 QMQEADISGYIPNGEWDLVGIPGKRSERFYECCKEPEYPDVTFTVTMRRRLYYGLNLLIP 240
 Db 181 QMQEADISGYIPNGEWDLVGIPGKRSERFYECCKEPEYPDVTFTVTMRRRLYYGLNLLIP 240
 QY 241 CVLISALALLVFLPADSGEKISLGITVLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
 Db 241 CVLISALALLVFLPADSGEKISLGITVLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVTVIVLQVHHDDPGGKMPKTRVILLNWCWFLRMKPGEDKVPACQHK 360
 Db 301 MIIVGLSVVTVIVLQVHHDDPGGKMPKTRVILLNWCWFLRMKPGEDKVPACQHK 360
 QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
 Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
 QY 421 LHGGQPEGDPDLAKILEEVRYIANRPRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 Db 421 LHGGQPEGDPDLAKILEEVRYIANRPRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 8
 AAB50016
 ID AAB50016 standard; Protein; 502 AA.
 AC AAB50016;
 XX
 DT 14-MAR-2001 (first entry)
 DE Mutant human alpha7 ligand gated ion channel #2.
 KW Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;
 XX 5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutein.
 OS Homo sapiens.
 XX Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 241
 FT /note= "Wild-type Cys substituted by Ser"
 XX
 PN WO200073431-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 25-MAY-2000; 2000WO-US11862.
 XX
 PR 27-MAY-1999; 99US-0136174.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Groppi VE, Wolfe ML, Berkenpas MB;
 XX
 DR WPI; 2001-061524/07.
 DR N-PSDB; AAC90386.
 XX
 PT Special cell culture medium for treating cells and for inducing
 PT mammalian cell lines to conduct calcium ions, comprising specified
 PT concentrations of ions of sodium, calcium and potassium at specified pH
 XX
 XX Claim 102; Pages 72-74; 77pp; English.
 PS

XX The present sequence is a mutant human alpha7 nicotinic acetylcholine
 CC gated ion channel. The human alpha7 ion channel was used in the
 CC construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand
 CC gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric
 CC ion channel can be expressed by recombinant cells in the present
 CC invention, resulting in preferential calcium ion conductance by the
 CC cells.

XX Sequence 502 AA;
 Query Match 59.8%; Score 300; DB 22; Length 502;
 Best Local Similarity 99.6%; Pred. No. 2.8e-282;
 Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRCSGGVWLAAASLLHVSLOGEFQRLKYLKELVKNYNPLRPVANDSQPLTVYFSL 60
 DB 1 MRCSGGVWLAAASLLHVSLOGEFQRLKYLKELVKNYNPLRPVANDSQPLTVYFSL 60
 QY 61 QIMDVDEKQVLTNTNIWLQMSWDTHYLQMNVSVEYPGVKTVPDQGIWKPDILLYNSADE 120
 DB 61 QIMDVDEKQVLTNTNIWLQMSWDTHYLQMNVSVEYPGVKTVPDQGIWKPDILLYNSADE 120
 QY 121 RFDATEFTNTLVNSSGHCQYLPPGIFKSSCYIDVRWPFDFVQHCKLKFGSWSYGGWSL 180
 DB 121 RFDATEFTNTLVNSSGHCQYLPPGIFKSSCYIDVRWPFDFVQHCKLKFGSWSYGGWSL 180
 QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVDTFTVTMRRLTYGLNLLIP 240
 DB 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVDTFTVTMRRLTYGLNLLIP 240
 QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
 DB 241 SVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVTVTVLQYHHHDPGGKMPKTRVILLNWCWFLRMKPGEDKVRPAQCHK 360
 DB 301 MIIVGLSVVTVTVLQYHHHDPGGKMPKTRVILLNWCWFLRMKPGEDKVRPAQCHK 360
 QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVCVPTPDGSGVCGRMACSPTHDEHL 420
 DB 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVCVPTPDGSGVCGRMACSPTHDEHL 420
 QY 421 LHGGOPPEGDPLAKILEEVRYIANFRFCODESEAVCSEWKFACVVDRLCLMAFSVFTI 480
 DB 421 LHGGOPPEGDPLAKILEEVRYIANFRFCODESEAVCSEWKFACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 9
 AAB50017
 ID AAB50017 standard; Protein; 502 AA.

AC AAB50017;

DT 14-MAR-2001 (first entry)

DE Mutant human alpha7 ligand gated ion channel #3.

KW Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;
 KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance; tutein.

XX Homo sapiens.

OS Synthetic.

TH Key Location/Qualifiers
 FT Misc-difference 230

FT /note= "Wild-type Thr substituted by Pro"

FT Misc-difference 241

FT /note= "Wild-type Cys substituted by Ser"

XX WO200073431-A2.
 XX 07-DEC-2000.
 XX 25-MAY-2000; 2000WO-US11862.
 XX 27-MAY-1999; 99US-0136174.
 XX (PHAA) PHARMACIA & UPJOHN CO.
 XX Groppi VE, Wolfe ML, Berkenpas MB;
 XX WPI; 2001-061524/07.
 DR N-PSDB; AAC90387.
 PT Special cell culture medium for treating cells and for inducing
 PT mammalian cell lines to conduct calcium ions, comprising specified
 PT concentrations of ions of sodium, calcium and potassium at specified pH
 PS Claim 104; Pages 75-77; 77pp; English.
 CC The present sequence is a mutant human alpha7 nicotinic acetylcholine
 CC gated ion channel. The human alpha7 ion channel was used in the
 CC construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand
 CC gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric
 CC ion channel can be expressed by recombinant cells in the present
 CC invention, resulting in preferential calcium ion conductance by the
 CC cells.

XX Sequence 502 AA;
 Query Match 45.6%; Score 229; DB 22; Length 502;
 Best Local Similarity 100.0%; Pred. No. 2.2e-213;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRCSGGVWLAAASLLHVSLOGEFQRLKYLKELVKNYNPLRPVANDSQPLTVYFSL 60
 DB 1 MRCSGGVWLAAASLLHVSLOGEFQRLKYLKELVKNYNPLRPVANDSQPLTVYFSL 60
 QY 61 QIMDVDEKQVLTNTNIWLQMSWDTHYLQMNVSVEYPGVKTVPDQGIWKPDILLYNSADE 120
 DB 61 QIMDVDEKQVLTNTNIWLQMSWDTHYLQMNVSVEYPGVKTVPDQGIWKPDILLYNSADE 120
 QY 121 RFDATEFTNTLVNSSGHCQYLPPGIFKSSCYIDVRWPFDFVQHCKLKFGSWSYGGWSL 180
 DB 121 RFDATEFTNTLVNSSGHCQYLPPGIFKSSCYIDVRWPFDFVQHCKLKFGSWSYGGWSL 180
 QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVDTFTVTMRRLTYGLNLLIP 229
 DB 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVDTFTVTMRRLTYGLNLLIP 229

RESULT 10
 AAB50014
 ID AAB50014 standard; Protein; 470 AA.

AC AAB50014;
 XX 14-MAR-2001 (first entry)

XX Chimeric alpha7/5-HT3 ligand gated ion channel.
 DE Murine; alpha7 nicotinic acetylcholine gated ion channel; human;
 KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutant.
 XX Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX WO200073431-A2.
 XX 07-DEC-2000.

XX 25-MAY-2000; 2000WO-US11862.
 XX 27-MAY-1999; 99US-0136174.
 XX (PHAA) PHARMACIA & UPJOHN CO.
 XX Groppi VE, Wolfe ML, Berkenpas MB;
 XX WPI; 2001-061524/07.
 XX N-PSDB; AAC90382.
 XX Special cell culture medium for treating cells and for inducing
 PT mammalian cell lines to conduct calcium ions, comprising specified
 PT concentrations of ions of sodium, calcium and potassium at specified pH
 PT .
 XX Claim 97; Pages 66-68; 77pp; English.
 XX The present sequence is a chimeric human alpha7 nicotinic
 CC acetylcholine/murine 5-hydroxytryptamine (5-HT3) ligand gated ion
 CC channel. The alpha7/5-HT3 chimeric ion channel can be expressed by
 CC recombinant cells in the present invention, resulting in preferential
 CC calcium ion conductance by the cells.
 XX Sequence 470 AA;
 SQ
 Query Match 44.6%; Score 224; DB 22; Length 470;
 Best Local Similarity 100.0%; Pred. No. 1.5e-208;
 Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRCSPGGVWALAAASLLHVSLSQGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
 Db 1 MRCSPGGVWALAAASLLHVSLSQGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
 QY 61 QIMDVDEKQVLTNTNIWLQSWTDHYLQNVSEYPGVKTFRPDGQIWKPDILLYNSADE 120
 Db 61 QIMDVDEKQVLTNTNIWLQSWTDHYLQNVSEYPGVKTFRPDGQIWKPDILLYNSADE 120
 QY 121 RFDATEFTNTVNVSSGHGCOYLPDGIKSSCYIDVRWPFDPVQCKLFGSGWSYGGWSL 180
 Db 121 RFDATEFTNTVNVSSGHGCOYLPDGIKSSCYIDVRWPFDPVQCKLFGSGWSYGGWSL 180
 QY 181 QMOEADISGYPNGEWDLVGIPGKRSERFYECCKEPYPDVTFV 224
 Db 181 QMOEADISGYPNGEWDLVGIPGKRSERFYECCKEPYPDVTFV 224
 RESULT 11
 AAB50018
 ID AAB50018 standard; Protein; 448 AA.
 XX AAB50018;
 AC
 XX 14-MAR-2001 (first entry)
 DT
 XX Mature cell surface chimeric alpha7/5-HT3 ligand gated ion channel.
 DE
 XX Murine; alpha7 nicotinic acetylcholine gated ion channel; human;
 KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutant.
 XX Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX WO2000073431-A2.
 PN
 XX 07-DEC-2000.
 PD
 XX 25-MAY-2000; 2000WO-US11862.
 PF
 XX 27-MAY-1999; 99US-0136174.
 PR
 XX (PHAA) PHARMACIA & UPJOHN CO.

XX Groppi VE, Wolfe ML, Berkenpas MB;
 XX WPI; 2001-061524/07.
 XX Special cell culture medium for treating cells and for inducing
 PT mammalian cell lines to conduct calcium ions, comprising specified
 PT concentrations of ions of sodium, calcium and potassium at specified pH
 PT .
 XX Disclosure; Fig 2; 77pp; English.
 XX The present sequence is the mature cell surface form of a chimeric human
 CC alpha7 nicotinic acetylcholine/murine 5-hydroxytryptamine (5-HT3) ligand
 CC gated ion channel (the full protein sequence is given in AAB50014). The
 CC alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells
 CC in the present invention, resulting in preferential calcium ion
 CC conductance by the cells.
 XX Sequence 448 AA;
 SQ
 Query Match 40.2%; Score 202; DB 22; Length 448;
 Best Local Similarity 100.0%; Pred. No. 3.2e-187;
 Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 23 GEFORKLYKELVKNYNPLRPVANDSQPLTVYFSLSLQIMDVDEKQVLTNTNIWLQSW 82
 Db 1 GEFORKLYKELVKNYNPLRPVANDSQPLTVYFSLSLQIMDVDEKQVLTNTNIWLQSW 60
 QY 83 TDHYLQNVSEYPGVKTFRPDGQIWKPDILLYNSADERPDATFTNTVNVSSGHGCOYLP 142
 Db 61 TDHYLQNVSEYPGVKTFRPDGQIWKPDILLYNSADERPDATFTNTVNVSSGHGCOYLP 120
 QY 143 PGIFKSSCYIDVRWPFDPVQCKLFGSGWSYGGWSLQMOEADISGYPNGEWDLVGIP 202
 Db 121 PGIFKSSCYIDVRWPFDPVQCKLFGSGWSYGGWSLQMOEADISGYPNGEWDLVGIP 180
 QY 203 GKRSEFYECCKEPYPDVTFV 224
 Db 181 GKRSEFYECCKEPYPDVTFV 202
 RESULT 12
 AAW12368
 ID AAW12368 standard; Protein; 502 AA.
 XX AAW12368;
 AC
 XX 17-JUN-1997 (first entry)
 DT
 XX Neuronal alpha-bungarotoxin binding protein alpha subunit.
 DE
 XX Neuronal alpha-bungarotoxin binding protein alpha 1; cholinergic;
 KW ligand binding; ion channel.
 XX Gallus sp.
 OS
 XX Key Location/Qualifiers
 FH Peptide 1..22
 FT /label= Sig_peptide
 FT Protein 23..502
 FT /label= Mat_protein
 XX US5599709-A.
 PN
 XX 04-FEB-1997.
 PD
 XX 28-SEP-1989; 89US-0413947.
 PF
 XX 28-SEP-1989; 89US-0413947.
 PR
 XX (SALK) SALK INST BIOLOGICAL STUDIES.
 PA

PI Lindstrom JM, Schoepfer RD;
 XX WPI: 1997-118297/11.
 DR N-PSDB; AAT59196.
 XX
 PT New isolated neuronal alpha-bungarotoxin-binding protein DNA - used
 PT to screen cholinergic agents and other drugs which may affect ligand
 PT binding, ion channel or other activities of the protein.
 XX
 PS Example; Fig 2A-B; 18pp; English.
 XX
 CC The alpha1 subunit (AAW12368) and alpha2 subunit (AAW12369) amino acid
 CC sequences of chick neuronal alpha-bungarotoxin binding protein
 CC (ABBP) were deduced from newly isolated DNA molecules (AAT59196-97)
 CC obt'd. from an 18-day chick embryo cDNA library. ABBP subunits can
 CC be produced in recombinant host cells, pref. a bacterium, and used
 CC in the screening of cholinergic agents and other drugs that may
 CC affect the ligand binding, ion channel or other activity of intact
 CC ABBP subtypes. The ABBP alpha1 and alpha2 subunits can also be
 CC used to produce subunit peptides for use as immunogens for
 CC preparing antibodies to permit affinity purification of subtypes
 CC and their histological location.
 XX
 SQ Sequence 502 AA;
 Query Match 18.3%; Score 92; DB 18; Length 502;
 Best Local Similarity 100.0%; Pred. No. 2e-80;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 275 FMLLVAEIMPATSDSVPLIAQYFASTMIIIVGLSVVTVIVLYHHDDPGGKMPKTRVI 334
 DB 275 FMLLVAEIMPATSDSVPLIAQYFASTMIIIVGLSVVTVIVLYHHDDPGGKMPKTRVI 334
 QY 335 LLNCAWFLMRKRPGEKVRPACQHKQRCSL 366
 DB 335 LLNCAWFLMRKRPGEKVRPACQHKQRCSL 366
 RESULT 13
 AAG74870
 ID AAG74870 standard; Protein; 63 AA.
 XX
 AC AAG74870;
 XX
 DT 03-SEP-2001 (first entry)
 XX
 DE Human colon cancer antigen protein SEQ ID NO:5634.
 XX
 KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW colorectal carcinoma; chromosome 15.
 XX
 OS Homo sapiens.
 XX
 PN WO200122920-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 28-SEP-2000; 2000WO-US26524.
 XX
 PR 29-SEP-1999; 99US-0157137.
 PR 03-NOV-1999; 99US-0163280.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Barash SC, Birse CE, Rosen CA;
 XX
 DR WPI: 2001-235357/24.
 DR N-PSDB; AAH34275.
 XX
 PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 PT useful for preventing, diagnosing and/or treating colorectal cancers -
 XX
 PS Claim 11; Page 7187; 9803pp; English.

XX
 CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where
 CC the proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene
 CC therapy and vaccine production. N and P may be used in the prevention,
 CC diagnosis and treatment of diseases associated with inappropriate P
 CC expression. For example, N and P may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of P by expressing
 CC inactive proteins or to supplement the patients own production of P.
 CC Additionally, N may be used to produce the colon cancer-associated Ps,
 CC by inserting the nucleic acids into a host cell and culturing the cell,
 CC to express the proteins. N and P can be used in the prevention, diagnosis
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
 CC and AAH77789 represent sequences used in the exemplification of the
 CC present invention.
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
 CC missing at time of publication, meaning no sequences are present for
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.
 XX
 SQ Sequence 63 AA;
 Query Match 9.4%; Score 47; DB 22; Length 63;
 Best Local Similarity 100.0%; Pred. No. 1.6e-37;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 456 VCSWKFAACVVDRLCLMAFSVFTIICITIGILMSAPNFVEAVSKDFA 502
 DB 17 VCSWKFAACVVDRLCLMAFSVFTIICITIGILMSAPNFVEAVSKDFA 63
 RESULT 14
 AAU83518
 ID AAU83518 standard; Protein; 70 AA.
 XX
 AC AAU83518;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Novel human ion channel ion-118.
 XX
 KW Ion channel; brain; mental disorder; human immunodeficiency virus;
 KW HIV; thyroid disorder; thyrotoxicosis; myxoedema; renal failure;
 KW inflammatory condition; Crohn's disease; rheumatoid arthritis;
 KW autoimmune disorder; movement disorder; CNS disorder; pain;
 KW neuropathic pain; migraine; headache; stroke; psychotic disorder;
 KW neurological disorder; anxiety; schizophrenia; dementia; dyskinesia;
 KW Huntington's disease; Tourette's syndrome; degenerative disorder;
 KW Parkinson's disease; Alzheimer's disease; ataxia; metabolic disorder;
 KW cardiovascular disease; diabetes; obesity; anorexia; hypotension;
 KW hypertension; thrombosis; atherosclerosis; proliferative disease;
 KW cancer; hyperproliferative disorder; psoriasis.
 XX
 OS Homo sapiens.
 XX
 PN WO200202639-A2.
 XX
 PD 10-JAN-2002.
 XX
 PF 05-JUL-2001; 2001WO-US21287.
 XX
 PR 05-JUL-2000; 2000US-215815P.
 PR 06-JUL-2000; 2000US-216479P.
 PR 06-JUL-2000; 2000US-216481P.
 PR 06-JUL-2000; 2000US-216482P.
 PR 10-JUL-2000; 2000US-217096P.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Benjamin CW, Roberts SL, Karnovsky AM, Ruble CL;
 XX
 DR WPI: 2002-140086/18.

DR N-PSDB; ABK33299.

XX Novel polynucleotide and polypeptides of human ion channels for

PT screening modulators useful for treating and diagnosing diseases e.g.

PT obesity, anorexia, anxiety, schizophrenia, dementia

XX

PS Claim 2; Page 94; 193pp; English.

XX The invention describes an isolated polynucleotide (I) comprising a

CC sequence encoding a polypeptide ion channel. The polypeptide (II) is

CC useful for inducing an immune response in a mammal against (II); and for

CC identifying a modulator of (II) activity. (I)/(II) are useful for

CC screening a human subject to diagnose a disorder affecting the brain

CC especially ion-channel related mental disorder genotype or its genetic

CC predisposition or identifying an ion channel allelic variant that

CC correlates with mental disorder, where a biological sample comprising

CC nucleic acid from human patient diagnosed with mental disorders or from

CC patients genetic progenitors or progeny is provided. Examples of the

CC disorders include disease and conditions as infections, such as viral

CC infections caused by human immunodeficiency virus (HIV); thyroid

CC disorders (e.g. thyrotoxicosis, myxoedema); renal failure; inflammatory

CC conditions (e.g. Crohn's disease); rheumatoid arthritis; autoimmune

CC disorders; CNS disorders (e.g. pain including neuropathic pain, migraine,

CC and other headaches); stroke; psychotic and neurological disorders

CC including anxiety, schizophrenia, dementia; dyskinesias, such as

CC Huntington's disease or Tourette's syndrome; degenerative disorders such

CC as Parkinson's, Alzheimer's; movement disorders, including ataxias;

CC metabolic and cardiovascular disease and disorders e.g. diabetes,

CC obesity, anorexia, hypotension, hypertension, thrombosis, and

CC atherosclerosis, proliferative disease and cancer and hyperproliferative

CC disorders such as psoriasis. This is the amino acid sequence of a novel

CC ion channel, described in the method of the invention.

XX

SQ Sequence 70 AA;

Query Match 9.0%; Score 45; DB 23; Length 70;

Best Local Similarity 100.0%; Pred. No. 1.5e-35;

Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 413 SPTHDHLHGQPPGPDPLAKILBEVRYIANFRQDSEAVC 457

Db 1 SPTHDHLHGQPPGPDPLAKILBEVRYIANFRQDSEAVC 45

RESULT 15

ABB76012

ID ABB76012 standard; Peptide; 32 AA.

AC ABB76012;

XX

DT 12-JUL-2002 (first entry)

XX

DE Beta amyloid binding peptide huma7.

XX

KW Beta amyloid; alpha 7 nicotinic acetylcholine receptor; nAChR;

KW receptor; human; Alzheimer's disease; antiparkinsonian;

KW analgesic; antidepressant; tranquilizer; neuroleptic; diagnosis;

KW therapy; drug screening.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Misc-difference 1..32 /note= "the peptide preferably contains at least

FT /note= "one D-form residue"

FT Modified-site 32 /note= "C-terminal amide"

FT

XX WO200214351-A2.

XX

PD 21-FEB-2002.

XX

PF 14-AUG-2001; 2001WO-US25410.

XX

PR 14-AUG-2000; 2000US-225048P.

XX

PA (ORTH) ORTHO-MCNEIL PHARM INC.

XX

PI Lee DHS, Reitz AB, Plata-Salaman C, Wang H;

XX

DR WPI; 2002-371643/40.

XX

PT New beta amyloid binding peptides, useful in the diagnosis of

PT Alzheimer's disease, Parkinson's disease or pain and in development of

PT high throughput screening, or computer-based rationale drug design to

PT create small molecule mimetics

XX

PS Claim 1; Page 36; 39pp; English.

XX

CC The present sequence is that of beta amyloid binding peptide

CC huma7 derived from the human alpha 7 nicotinic acetylcholine

CC receptor (nAChR). The peptide, which is preferably N-acetylated

CC and C-amidated, can be synthetically produced using D or L isomeric

CC amino acid precursors. It is one of a set of claimed beta amyloid

CC binding peptides (see ABB75988-ABB76015). These peptides can be

CC used in a method for diagnosing Alzheimer's disease (AD) by binding

CC to beta amyloid. This enables the measurement of free beta

CC amyloid(1-40) or beta amyloid(1-42) present in biological tissues

CC or fluids in AD patients, or those in the early stages of AD, or who

CC will develop AD in the future. The binding reaction of these

CC peptides and beta amyloid can also be used in drug screening assays

CC to identify small molecule modulators of alpha 7 nAChR for treating

CC neurodegenerative disorders such as AD, Parkinson's disease, pain,

CC neuropathic pain, depression, anxiety, obsessive compulsive

CC behaviour, phobia, post-traumatic stress, panic, schizophrenia,

CC psychosis, bipolar disorder, dementia and substance abuse. The

CC claimed peptides can also be therapeutically active agents, or

CC can be used to model interactions with beta amyloid for rational

CC drug design. Hum7 peptide attenuated beta amyloid's inhibition

CC of potassium-evoked acetylcholine release from rodent synaptosomes

CC (IC50 = 0.362 uM). Acetylcholine release inhibition at 100 uM was

CC 90%. Huma7 peptide also inhibited 125I-beta amyloid binding to

CC alpha 7 SK-N-MC membranes and beta amyloid(1-32) deposition onto

CC synthaloid plates.

XX

SQ Sequence 32 AA;

Query Match 6.4%; Score 32; DB 23; Length 32;

Best Local Similarity 100.0%; Pred. No. 3.2e-23;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 NGEWDLVGIGKRSERFECCKEPYDVTFTV 224

Db 1 NGEWDLVGIGKRSERFECCKEPYDVTFTV 32

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